

Tue Nov 23 09:18:29 2004

US-09-705-500a-3.rni

Page 1

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 22, 2004, 18:05:37 ; Search time 95 Seconds  
(without alignments)  
1848.051 Million cells updates/sec

Title: US-09-705-500A-3  
Perfect score: 1268  
Sequence: 1 MGNNAVLIVYISATHE.....NARGEDSPSHIKRSHESA 247

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Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-DB=Issued Patents NA -QFMT=fastap -SUFFIX=rni -MINMATCH=0.1 -LOOPEL=0  
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blsum62 -TRANS=human40.cdi  
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-DEF TIMEOUT=120 -MARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -DELOP=6 -DELEXT=7

Database :

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2: /cgn2\_6/prodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/prodata/1/ina/6A\_COMB.seq:\*  
4: /cgn2\_6/prodata/1/ina/6B\_COMB.seq:\*  
5: /cgn2\_6/prodata/1/ina/6CTUS\_COMB.seq:\*  
6: /cgn2\_6/prodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

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1	1268	100.0	771	2	US-09-361-736B-1
2	1268	100.0	771	2	US-09-193-881-2
3	1268	100.0	771	2	US-09-193-881-3
4	1268	100.0	771	2	US-09-193-881-4
5	1268	100.0	771	2	US-09-193-881-5
6	1268	100.0	771	2	US-09-193-881-6
7	1268	100.0	771	2	US-09-193-881-7
8	1268	100.0	771	2	US-09-193-881-8
9	1268	100.0	771	2	US-09-193-881-9
10	1268	100.0	771	2	US-09-193-881-10
11	1268	100.0	771	2	US-09-193-881-11
12	1268	100.0	771	2	US-09-193-881-12

13	352	27.8	892	4	US-09-361-736B-1	Sequence 1, Appl1
14	214	16.9	257	4	US-09-193-881-2	Sequence 2, Appl1
15	155	12.2	246	4	US-09-193-881-3	Sequence 3, Appl1
16	143.5	11.3	339	4	US-09-621-976-12801	Sequence 12801, A
17	98	7.7	285	4	US-09-193-881-1	Sequence 1, Appl1
18	93.5	7.4	3253	4	US-09-710-279-3955	Sequence 3955, Ap
19	93.5	7.4	30549	3	US-09-134-001C-322	Sequence 322, App
20	91	7.2	4348	4	US-09-828-062-5	Sequence 5, Appl1
21	90	7.1	1384	4	US-09-227-357-142	Sequence 142, App
22	86	6.8	1947	4	US-09-270-767-10718	Sequence 10718, A
23	86	6.8	1230025	4	US-09-198-452A-1	Sequence 1, Appl1
24	85.5	6.7	936	4	US-09-710-279-2459	Sequence 2459, Ap
25	85.5	6.7	1971	3	US-09-134-001C-1485	Sequence 1485, Ap
26	85.5	6.7	2818	4	US-09-762-724-7	Sequence 3447, Ap
27	84	6.6	10136	5	PCT-US95-16216-2	Sequence 2, Appl1
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29	83.5	6.6	1000	4	US-09-655-908-7	Sequence 7, Appl1
30	83.5	6.6	1071	4	US-09-655-908-5	Sequence 5, Appl1
31	83.5	6.6	3084	4	US-09-762-724-7	Sequence 7, Appl1
32	83.5	6.6	3090	4	US-09-762-724-5	Sequence 5, Appl1
33	83	6.5	795	4	US-09-134-000C-2426	Sequence 2426, Ap
34	83	6.5	960	4	US-09-710-279-791	Sequence 791, App
35	83	6.5	960	4	US-09-710-279-2007	Sequence 2007, Ap
36	83	6.5	1197	4	US-09-710-279-43	Sequence 43, Appl1
37	83	6.5	1197	4	US-09-710-279-1497	Sequence 1497, App
38	83	6.5	1254	3	US-09-134-001C-973	Sequence 973, App
39	83	6.5	1254	3	US-09-134-001C-973	Sequence 4053, Ap
40	83	6.5	3314	4	US-09-710-279-3745	Sequence 3745, Ap
41	83	6.5	3314	4	US-09-710-279-3745	Sequence 3746, Ap
42	83	6.5	3393	4	US-09-710-279-4085	Sequence 4085, Ap
43	83	6.5	3885	4	US-09-710-279-3883	Sequence 3883, Ap
44	82	6.5	1089	3	US-09-134-001C-1833	Sequence 1833, Ap
45	82	6.5	4411529	3	US-09-103-840A-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-08-208-005C-1  
; Sequence 1, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Copuscles of Stannius Protein, Stannocalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208,005C  
; FILING DATE: 8 MARCH 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 1:  
; Sequence 1, Appl1



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Qy      121 ILeaGluValGInGluGluCySerLeuLeuValCysSerIleAlaValArg 140
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Qy      161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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Qy      181 SerLeuValGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
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Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
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Qy      241 ArgThrSerHisGluSerAla 247
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RESULT 3
US-08-431-117A-1
; Sequence 1, Application US/08431117A
; Patent No. 5994301
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stanniocalcin
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GIUFFILIAN,
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,117A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/208,005
; FILING DATE: 8 MARCH 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: FERRARO, GREGORY D.
; REGISTRATION NUMBER: 36,134
; REFERENCE/DOCKET NUMBER: 325800-296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: cDNA

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US-08-431-117A-1
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy      41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db      136 GAAGTGTTCGTTGCTCAACAGTCTTCAACAGTCCGCGGCTTTGCATGCTG 195
Qy      61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
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Qy      81 AlaIleLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      256 GCTGCTAAATTTGACACTCAGGAAAGCAATTCCTCAAGAGACTTAAATGCAATGCC 315
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Qy      121 ILeaGluValGInGluGluCySerLeuLeuValCysSerIleAlaValArg 140
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US-09-023-655-1502
; Sequence 1502, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: COCKE, BENJAMIN G.
; APPLICANT: COCKE, BENJAMIN G.
; APPLICANT: SUSAN G. STUART
; APPLICANT: JEFFREY J. SEILHAMER
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE

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QY 225 LeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys----- 240
Db 742 GCCAAGCAGAGTCCAGAGGTGAGCGAGGAGCAAAAGCCACCGAATGCCATGCTCGA 801
QY 241 ---ArgThrSerHisGluSerAla 247
Db 802 GGCAGAACCGGTGCGCAGAGCGCT 825

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Sawislak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6672
TELEFAX: 206-442-6678
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 906 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 1..72
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 73..906
FEATURE:
NAME/KEY: CDS
LOCATION: 1..906
US-08-831-132-1
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Query Match: 27.92% Indels: 12
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QY 22 Glu---GluAsnAspSerValSerProArgLysSerArgValAlaAlaGluAsnSerAla 40
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QY 41 GluValValArgCysLeuAsnSerAlaLeuGluValGlyCysGlyAlaPheAlaCysLeu 60
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QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 214 GAGAACAACTCTTGTGAGATTCGGGGCTTACATGGGATTTGCATGACTTTTTCGACAAAC 273
QY 81 AlaAlaLysPheAspThrGlnGlyLysValAlaPheValLysGluSerLeuLysCysIleAla 100
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QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 394 GTGTCCAGTTGACCGGGAATGTACTACCTCAACAGCAGACCTGTCGCGCTGCGCAGAG 453
QY 141 AspProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 454 AACACCCCGGTGATGTGAGATGATCATTTCAAGACCTTGTCTGCTGCAAGAACCTTAC 513

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RESULT 7  
 US-08-831-132-1  
 Sequence 1, Application US/08831132  
 Patent No. 6088322  
 GENERAL INFORMATION:  
 APPLICANT: Kuestner, Rolf E.  
 APPLICANT: Conklin, Darrell C.  
 APPLICANT: Lok, Si  
 APPLICANT: Biddle, Michele  
 APPLICANT: Downey, William  
 TITLE OR INVENTION: STANNIOCALCIN-2  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: ZymoGenetics, Inc.  
 STREET: 1201 Eastlake Avenue East  
 CITY: Seattle  
 STATE: WA  
 COUNTRY: USA  
 ZIP: 98102  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk



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; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: human
US-09-361-736B-11

Alignment Scores:
Pred. No.: 3,74e-38      Length: 1024
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 4                   Gaps: 4

US-09-705-500A-3 (1-247) x US-09-361-736B-11 (1-1024)

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DB 109 CTGGCTTTGGTGTGGTGGCCACCTTTGACCCGGCGGGGAGACCGACCCCAACCCACC 168
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 169 GAGGGTCCCCAAGACAGAGAGCTCCACAGAAAGGCGCGCTGTCCCTCGAGAAATACAGCG 228
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 229 GAGATCCAGACAGCTGTGTGTGCAACGCTGGCGAGTGTGGGTGGCTGTGTAATGTTTC 288
QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLeuSerPheLeuTyrSer 80
DB 289 GAGAACACCTCTGTAGATTCGGGGCTTACATGGAATTTGATGACTTTTCTGCACAC 348
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
DB 349 GCTGGAAATTTGATGATCCCGACAGGCAAGTCAATCATAAAGCGCTTGAAATGTAAAGCC 408
QY 101 AsnGlyValIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 409 CAGCTCTGGGACACAGGTTCCGGCTCATAGCCGGAAGTCCCGCCATCCAGGAATG 468
QY 121 IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 469 GTGTCCAGATTGACGCGGAGATCTACTCAAGCAGACAGCTGTGCGGCTCCACAGAG 528
QY 141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
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DB 703 TTTCGACCTCGGC-CATCCAGAAGCTCCACAGCGGCCCGCCGAGCGCCACCCCAAGT 761
QY 221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGlnGluAspSerPro 236
DB 762 GGAAGAACCAAGCTCTCCAGGCCCCACACCGGGGAGAGAGACATCACT 812

RESULT 10
US-09-193-881-11
; Sequence 11, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen

```

```

; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; TITLE OF INVENTION: Breast
; FILE REFERENCE: 6248-US-P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 11
; LENGTH: 1756
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-11

Alignment Scores:
Pred. No.: 9.17e-38      Length: 1756
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
DB: 4                   Gaps: 4

US-09-705-500A-3 (1-247) x US-09-193-881-11 (1-1756)

QY 9 LeuValIeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB 102 CTGGCTTTGGTGTGGTGGCCACCTTTGACCCGGCGGGGAGACCGACCCCAACCCACC 161
QY 22 Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB 162 GAGGGTCCCCAAGACAGAGAGCTCCACAGAAAGGCGCGCTGTCCCTCGAGAAATACAGCG 221
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB 222 GAGATCCAGACAGCTGTGTGTGCAACGCTGGCGAGTGTGGGTGGCTGTGTAATGTTTC 281
QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB 282 GAGAACACCTCTGTGATTCGGGGCTTACATGGAATTTGATGACTTTTCTGCACAC 341
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
DB 342 GCTGGAAATTTGATGATCCCGACAGGCAAGTCAATCATAAAGCGCTTGAAATGTAAAGCC 401
QY 101 AsnGlyValIleThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB 402 CAGCTCTGGGACACAGGTTCCGGCTCATAGCCGGAAGTCCCGCCATCCAGGAATG 461
QY 121 IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB 462 GTGTCCAGATTGACGCGGAGATCTACTCAAGCAGACAGCTGTGCGGCTCCACAGAG 521
QY 141 AspProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB 522 AACACCCGGGTGATGTGAGATGATCATTTCAAGCACTTGCTGTGCACAAACCTTC 581
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
DB 582 GTGAGCTCGTGAATTGCTGTGACCTGTGGGAGAGAGTGAAGAGGCCATCACCCAC 641
QY 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB 642 AGGGTCAAGTTAGTGAAGACAGAACTGGGAGAGCTGTGCTCCACTTGG-----AGC 695
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlnProGln 220
DB 696 TTTCGACCTCGGC-CATCCAGAAGCTCCACAGGCGGCCCGGAGCGCCACCCCAAGT 754

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QY      221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
DB      755 GGACAGAACCAAGCTCTCCAGGGCCCAACGAGGAGACGACATCACCCT 805

RESULT 11
US-09-193-881-10
; Sequence 10, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Coldits
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248.US.P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; NUMBER OF SEQ. ID NOS: 29
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 1760
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-10

Alignment Scores:
Pred. No.:      9.21e-38      Length:      1760
Score:          354.00      Matches:      82
Percent Similarity: 52.32%      Conservative: 42
Best Local Similarity: 34.60%      Mismatches: 102
Query Match:    27.92%      Indels:      12
DB:              4          Gaps:          4

US-09-705-500a-3 (1-247) x US-09-193-881-10 (1-1760)

QY      9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB      105 CTGGCTTGGTGTGTGGACACCTTTGACCGCGCGGGGACCGACCCCAACCCACC 164

QY      22 Gln---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
DB      165 GAGGGTCCCCCAAGACAGAGCTCCAGCAAGAAAGCGCGCTGTCTGCAGATACAGCG 224

QY      41 GlnValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLeu 60
DB      225 GAGATCCAGACTGTGTGTGCAACGCTGGCGAGATGGGGTGTGGCTGTTCGAAATGTTTC 284

QY      61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB      285 GAGACAACTCTGTGAGATTGGGGCTTACATGATTTGCATGACTTTTCGCAACAC 344

QY      81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuTyrCysIleAla 100
DB      345 GCTGGAATAATTATATGCCAGGGGCAAGTCACTTCAATAAGACGCTTGAAATGTAAGGCC 404

QY      101 AsnGlyValThrSerIysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB      405 CAGGCTCTGGGACAGGTTCCGCTCGCATTAAGCCGGAAGTCCCGGCCCATCGAGGAATG 464

QY      121 IleAlaGluValGlnGluGluCysTyrSerIysLeuAsnValCysSerIleAlaLysArg 140
DB      465 GTGTCCCAAGTTGACGGGGAATGCTACCTCAACACAGCACTGTGCGCGGCTGCCAGAG 524

QY      141 AspProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB      525 AACACCCCGGGTATATGAGGATGATGCATTTCAAGAGACTGTGTGACAGCAACCCCTAC 584

QY      161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
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DB      585 GTGACCTCGTGTGACCTTCTGCTGACCTGTGGGAGAGAGTGAAGAGCCATACCCAC 644
QY      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB      645 AGCTGCGAGCTTTCAGTGTGAGACAGACTGGGGAAGCCTGTGCTCATCTTG-----AGC 696
QY      201 HisCysAlaGlnThrHisPheArgAlaAspPheAsnArgArgTyrThrAsnGluProGln 220
DB      699 TTCTGACCTCGGC-CATCCAGAGCTTCCACAGCGCCGCCCGCCAGGCCACCCCAAGT 757

QY      221 LysLeuLysValLeuLeuArgAsn---LeuArgGlyGluGluAspSerPro 236
DB      758 GGACAGAACCAAGCTCTCCAGGGCCCAACGAGGAGACGACATCACCCT 808

RESULT 12
US-08-460-529B-1
; Sequence 1, Application US/08460529B
; Patent No. 5994103
; GENERAL INFORMATION:
; APPLICANT: OLSEN, ET AL.
; TITLE OF INVENTION: Human stemlocalcin-alpha
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
; ADDRESSEE: CECCHI, STEWART & OLSTEIN
; STREET: 6 BECKER FARM ROAD
; CITY: ROSELAND
; STATE: NEW JERSEY
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 INCH DISKETTE
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WORD PERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/460,529B
; FILING DATE: June 2, 1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/13206
; FILING DATE: 10 NOV 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: MULLINS, J.G.
; REGISTRATION NUMBER: 33,073
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 892 BASE PAIRS
; TYPE: NUCLEIC ACID
; STRANDEDNESS: SINGLE
; TOPOLOGY: LINEAR
; MOLECULE TYPE: CDNA
US-08-460-529B-1

Alignment Scores:
Pred. No.:      5.57e-38      Length:      892
Score:          352.00      Matches:      81
Percent Similarity: 52.94%      Conservative: 45
Best Local Similarity: 34.03%      Mismatches: 101
Query Match:    27.76%      Indels:      12
DB:              2          Gaps:          4

US-09-705-500a-3 (1-247) x US-08-460-529B-1 (1-892)

QY      9 LeuValLeuValIleSer-----AlaSerAlaThrHisGluAla 21
DB      115 CTGGCTTGGTGTGTGGACACCTTTGACCGCGCGGGGAGACCGACGACCAACCCACC 174
```

```
QY      22  Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
      175  GAGGATCCCAAGACAGAGAGCTCCACAGCAAAAGCGCTGCTCCTCGACAAATACAGG 234
      41  GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
      235  GAGATCCAGACAGCTTTGGTCAACGCTGCGAGATGGGGGTGGGCTGTTCATTAATGTTTC 294
      61  GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
      295  GAGAACAACTCTTGATGATTCGGGGCTTTCATGCGATTTGATGACTTTTTCGACAAAC 354
      81  AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
      355  GCTGAAAATTGATGATCCCGCAAGTCATTCATCAAGACGCTTGAATGTAAGGCG 414
      101  AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
      415  CACGCTCGGCGACAGGTTTCGCTGCATTAAGCCGGAAGTCCCGGCGCATCAGGAAATG 474
      121  IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
      475  GTGTCCCAAGTGGAGGGGGAATGCTACCTCAAGACAGACCTGTGGCGGCTGCCAGAG 534
      141  AsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
      535  AACACCCGGGTGATGATGAGATGATTCATTCCAGAGCTTGTCTGACCAACCCCTAC 594
      161  AsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIleArgAsp 180
      595  GTGACCTCTCTGAACCTTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATCAACCCAC 654
      181  SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
      655  AGCGTGAGGTTCAAGTGTGACAGCAAACTGGGGAAGCTGTGCTCCATCTTG-----AGC 708
      201  HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlnProGln 220
      709  TTCGCACTCCGA-CATCCAGAAAGCTCCACGCGGCCCGCCAGGCCACGCCAGGT 767
      221  LysLeuLysValLeuLeuArgAsn---LeuArgGlyGlnGlnAspSerProSer 237
      768  GGACAGAACCAAGCTCTCCAGGGCCACACCGGGGGAAGAGACATCACTCC 821

RESULT 13
US-09-361-736B-1
; Sequence 1, Application US/09361736B
; Patent No. 661877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Staminalc1n-Alpha
; FILE REFERENCE: PRI43P1D1
; CURRENT APPLICATION NUMBER: US/09361,736B
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 892
; TYPE: DNA
; ORGANISM: human
US-09-361-736B-1

Alignment Scores:
Pred. No.: 5,57e-38 Length: 892
Score: 352.00 Matches: 81
Percent Similarity: 52.94% Conservative: 45
Best Local Similarity: 34.03% Mismatches: 101
Query Match: 27,76% Indels: 12
DB: 4 Gaps: 4
```

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US-09-705-500A-3 (1-247) x US-09-361-736B-1 (1-892)
QY      9  LeuValLeuValIleSer-----AlaSerAlaThrHisGlnAla 21
      115  CTGGCTTTGGTGGTGGACCTTTGACCCGCGGGGAGCCAGCAGCAGCAACCCACC 174
      22  Glu---GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
      175  GAGGATCCCAAGACAGAGAGCTCCACAGCAAAAGCGCTGCTCCTCGACAAATACAGG 234
      41  GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
      235  GAGATCCAGACAGCTTTGGTCAACGCTGCGAGATGGGGGTGGGCTGTTCATTAATGTTTC 294
      61  GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
      295  GAGAACAACTCTTGATGATTCGGGGCTTTCATGCGATTTGATGACTTTTTCGACAAAC 354
      81  AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
      355  GCTGAAAATTGATGATCCCGCAAGTCATTCATCAAGACGCTTGAATGTAAGGCG 414
      101  AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
      415  CACGCTCGGCGACAGGTTTCGCTGCATTAAGCCGGAAGTCCCGGCGCATCAGGAAATG 474
      121  IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
      475  GTGTCCCAAGTGGAGGGGGAATGCTACCTCAAGACAGACCTGTGGCGGCTGCCAGAG 534
      141  AsnProGlnAlaIleThrGlnValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
      535  AACACCCGGGTGATGATGAGATGATTCATTCCAGAGCTTGTCTGACCAACCCCTAC 594
      161  AsnArgLeuValArgSerLeuLeuGluCysAspGlnAspThrValSerThrIleArgAsp 180
      595  GTGACCTCTCTGAACCTTGCTGACCTGTGGGAGAGAGTGAAGAGGCCATCAACCCAC 654
      181  SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
      655  AGCGTGAGGTTCAAGTGTGACAGCAAACTGGGGAAGCTGTGCTCCATCTTG-----AGC 708
      201  HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlnProGln 220
      709  TTCGCACTCCGA-CATCCAGAAAGCTCCACGCGGCCCGCCAGGCCACGCCAGGT 767
      221  LysLeuLysValLeuLeuArgAsn---LeuArgGlyGlnGlnAspSerProSer 237
      768  GGACAGAACCAAGCTCTCCAGGGCCACACCGGGGGAAGAGACATCACTCC 821

RESULT 14
US-09-193-881-2
; Sequence 2, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: Breast
; CURRENT APPLICATION NUMBER: US/09/193,881A
; PRIOR FILING DATE: 1998-11-18
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 257
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-2

Alignment Scores:
Pred. No.: 4.73e-20 Length: 257
Score: 214.00 Matches: 34
Percent Similarity: 69.41% Conservative: 25
Best Local Similarity: 40.00% Mismatches: 26
Query Match: 16.88% Indels: 0
DB: 4 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-193-881-2 (1-257)

QY PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
Db 2 TTGGAATGTTCCAGAAACAACCTCTGTGAGATTCGGGGCTTACATGGATTTCATGACT 61

QY PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
Db 62 TTCTGCACAAACCTGGAAATTGATGCCACGGCAAGTCTCATCAAAAGACGCTTG 121

QY LysCysrIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThr 116
Db 122 AAATGTAAAGCCCAAGCTGCGGCACAGGTTGCGCTGCATTAAGCCGAAAGTCCCGGCC 181

QY PheGlnArgMetIleAlaGluValGlnGluCysTyrSerLysLeuAsnValCysSer 136
Db 182 ATCAGGGAATGATGCTCCAGTTGTCAGCGGAAATGCTACTCAAGCAGCAGCCTGTGCGG 241

QY 137 ILeAlaLysArgAsn 141
Db 242 GCTGCCAGGAGAAC 256

RESULT 15
US-09-193-881-3
; Sequence 3, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klass
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248 US, P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 246
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-193-881-3

Alignment Scores:
Pred. No.: 4.93e-12 Length: 246
Score: 155.00 Matches: 27
Percent Similarity: 62.67% Conservative: 20
Best Local Similarity: 36.00% Mismatches: 24
Query Match: 12.22% Indels: 4
DB: 4 Gaps: 1

US-09-705-500A-3 (1-247) x US-09-193-881-3 (1-246)

QY 83 LysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysrIleAlaAsnGly 102
Db 6 AAATTGATGCCAGGCAAGTCTTATCAAAAGACCCCTTGAATGTAAAGGCCACGCT 65
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```
QY ValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMetIleAla 122
Db 66 CTGCGGCACAGGTTGCGCTGCATTAAGCCGGAAGTCCCGGCCCATCAGGAAATGTGTCC 125

QY 123 GluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArgAsnPro 142
Db 126 CAGTTGCAGCCGGGAATGCTACCTCAAGCAGCAGCCTGTGCCGCTGCCAGAGAACACC 185

QY 143 GluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsn 157
Db 186 CCGGTGATAGTGAATGATC-----CATTTCAAGAAC 218

Search completed: November 22, 2004, 18:13:35
Job time : 129 secs
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: November 22, 2004, 18:09:53 ; Search time 524 Seconds

(without alignments)  
2547.128 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3627888 seqs, 2701811610 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOPFC=0 -LOPEXT=0 -UNIT=bits -START=1 -END=1 -MATRIX=biosum62  
-TRANS=human40.ccl -LIST=45 -DOCALIGN=200 -THR\_SCORE=pct -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=JOCL -OUTFMT=p1c -NOR=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US09705500 @cgn 1 1 575 @rnucat 22112004 073749 19909  
-NCU=6 -ICPU=3 -NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100  
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPO=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database: Published Applications NA:

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3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09B\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09C\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10A\_PUBCOMB.seq:\*  
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19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1268	100.0	771	13	US-10-416-05T-1	Sequence 1, Appl1
2	1268	100.0	1283	18	US-09-844-989A-1	Sequence 1, Appl1
3	1268	100.0	1283	18	US-10-614-990A-1	Sequence 1, Appl1
4	1268	100.0	3757	14	US-10-641-642-1582	Sequence 1502, Ap
5	1268	100.0	3756	13	US-10-044-090-638	Sequence 638, App
6	1268	100.0	3897	14	US-10-198-845-13651	Sequence 13651, A
7	1268	100.0	3901	15	US-10-177-293-470	Sequence 440, App
8	1268	100.0	3901	15	US-10-465-522-17	Sequence 17, Appl
9	1268	100.0	3901	16	US-10-159-563-292	Sequence 292, App
10	1268	100.0	3901	16	US-10-372-683-40	Sequence 40, Appl
11	1268	100.0	3901	16	US-10-240-925-1425	Sequence 1425, Ap
12	1250	98.6	2572	9	US-09-925-900-486	Sequence 486, App
13	861	67.9	585	9	US-09-778-320-149	Sequence 149, App
14	861	67.9	585	9	US-09-910-689-149	Sequence 149, App
15	861	67.9	585	13	US-10-010-742-149	Sequence 149, App
16	861	67.9	585	17	US-10-714-389-149	Sequence 149, App
17	861	67.9	585	17	US-10-717-296-149	Sequence 149, App
18	689	54.3	473	14	US-10-060-036-2677	Sequence 2677, Ap
19	508	40.1	420	9	US-09-778-320-141	Sequence 141, App
20	508	40.1	420	9	US-09-910-689-141	Sequence 141, App
21	508	40.1	420	13	US-10-010-742-141	Sequence 141, App
22	508	40.1	420	17	US-10-714-389-141	Sequence 141, App
23	508	40.1	420	17	US-10-717-296-141	Sequence 141, App
24	396	31.2	436	10	US-09-918-595-33032	Sequence 33032, A
25	380	30.0	560	15	US-10-029-386-9487	Sequence 9487, Ap
26	370	28.2	219	9	US-09-864-761-21309	Sequence 21309, A
27	363	28.6	215	15	US-10-029-386-23167	Sequence 23167, A
28	354	27.9	1024	15	US-10-418-226-11	Sequence 11, Appl
29	354	27.9	1756	9	US-09-193-881-11	Sequence 11, Appl
30	354	27.9	1756	15	US-10-338-395-11	Sequence 11, Appl
31	354	27.9	1760	9	US-09-193-881-10	Sequence 10, Appl
32	354	27.9	1760	15	US-10-338-395-10	Sequence 10, Appl
33	354	27.9	1837	15	US-10-364-889-3	Sequence 3, Appl1
34	354	27.9	1837	16	US-10-058-270A-21	Sequence 21, Appl
35	354	27.9	2380	10	US-09-918-624B-54	Sequence 54, Appl
36	354	27.9	2380	15	US-10-177-293-442	Sequence 442, App
37	354	27.9	2380	15	US-10-172-118-946	Sequence 946, App
38	354	27.9	2380	15	US-10-295-027-99	Sequence 99, Appl
39	354	27.9	2380	16	US-10-173-999-79	Sequence 79, Appl
40	354	27.9	2380	16	US-10-159-563-109	Sequence 109, App
41	354	27.9	2380	16	US-10-382-887-946	Sequence 946, App
42	354	27.9	2759	14	US-10-198-846-9993	Sequence 9993, App
43	354	27.9	4173	13	US-10-071-766-128	Sequence 128, App
44	352	27.8	892	9	US-09-361-736-1	Sequence 1, Appl1
45	352	27.8	892	15	US-10-418-226-1	Sequence 1, Appl1

## ALIGNMENTS

RESULT 1  
US-10-116-051-1  
; Sequence 1, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: COMPOUNDS OF STANNIUS PROTEIN, STANNIOCALCIN  
; FILE REFERENCE: PFI08PDI01  
; CURRENT APPLICATION NUMBER: US/10/116, 051  
; CURRENT FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 771  
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-10-116-051-1

Alignment Scores:
Pred. No.: 7.23e-166 Length: 771
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 13 Gaps: 0

US-09-705-500a-3 (1-247) x US-10-116-051-1 (1-771)

Cy 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
Db 16 ATGCTCCAAACACAGAGAGCTTCTGCTGCTGATGATGCTCTTCCAAACCATAG 75
Cy 21 AlAGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 76 GCGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAACTCAGCT 135
Cy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValIGlyCysGlyValAlaPheAlaCysLeu 60
Db 136 GAAAGTGTCTGCTGCTCCAAACAGTCTTACAGTGGCTGGCGGCTTTTGCATGCTG 195
Cy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 196 GAAACCTCCACCTGTGACAGATGGATGTATGACATCTGTAAATCTTCTGTACAGC 255
Cy 81 AlaAlaLysPheAspThrGlnGlyValAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 256 GCTGCTAAATTTCACACTCAGGAAAGCAATGCTGCAAGAGAGCTTAAATGCACTGCC 315
Cy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 316 AACGGGCTCACCTCCAAAGCTTCTTCGCGCATTCGAGAGTGGCTCCACTTCCAAAGAGT 375
Cy 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 376 ATGGCTGAGGTGAGAGAGAGTCTCTACAGCAAGCTAAATGTGCGAGCATCCGCAAGCG 435
Cy 141 AsnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 436 AACCTGGAAGCCATCACTGAGTGTCTGCAAGCTCCCAATCACTTCCAAACAGATCAT 495
Cy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 496 AACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACAGTCCAGCAATCCAGAGC 555
Cy 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 556 AGCTGATGAGAAATTTGGGCTTAACATGCGCAAGCTCTTCCACATCTTGCAGACAGAC 615
Cy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db 616 CACTGTGCGCAACACACCCACAGAGCTGACTTCACAGAGAGCGCCCATATAGCGCGAG 675
Cy 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
Db 676 AAGGTGAAGTCTCTCCAGGAACCTCCGAGTGAAGAGACTTCTCTCCCAATCAAA 735
Cy 241 ArgThrSerHisGluSerAla 247
Db 736 CGCAGATCCCATGAGAGTGCA 756

RESULT 2
US-09-840-989A-1
; Sequence 1, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannicalcain Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2

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; CURRENT APPLICATION NUMBER: US/09/840,989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc feature
; LOCATION: (1254)..(1254)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; NAME/KEY: misc feature
; LOCATION: (1279)..(1279)
; OTHER INFORMATION: n is equal to a, t, c, or g.
US-09-840-989A-1

Alignment Scores:
Pred. No.: 1.7e-165 Length: 1283
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 9 Gaps: 0

US-09-705-500a-3 (1-247) x US-09-840-989A-1 (1-1283)

Cy 1 MetLeuGlnAsnSerAlaValLeuValLeuValIleSerAlaSerAlaThrHisGlu 20
Db 45 ATGCTCCAAACACAGAGAGCTTCTGCTGCTGATGATGCTCTTCCAAACCATAG 104
Cy 21 AlAGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 105 GCGGAGCAGAAATGACTCTGTGAGCCCCAGGAAATCCCGAGTGGCGGCCCAAACTCAGCT 164
Cy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValIGlyCysGlyValAlaPheAlaCysLeu 60
Db 165 GAAAGTGTCTGCTGCTCCAAACAGTCTTACAGTGGCTGGCGGCTTTTGCATGCTG 224
Cy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 225 GAAACCTCCACCTGTGACAGATGGATGTATGACATCTGTAAATCTTCTGTACAGC 284
Cy 81 AlaAlaLysPheAspThrGlnGlyValAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 285 GCTCTAAATTTCACACTCAGGAAAGCAATGCTCAAAAGAGCTTAAATGCAATCCATGCC 344
Cy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 345 AACGGGCTCACCTCCAGAGCTTCTTCCGCAATTCGAGAGTCTTCCAAAGAGT 404
Cy 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 405 ATTGCTGAGGTGAGAGAGTGTCTACAGAGTGTATGTGCGAGCATCCGCAAGCGG 464
Cy 141 AsnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 465 AACCTGGAAGCCATCACTGAGTGTCTCAGTGGCCCAATCACTTCCAAACATCACTAT 524
Cy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 525 AACAGACTTGTCCGAAGCTGCTGGAATGTGATGAAGACACAGTCCAGCAATCCAGAGAC 584

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QY 181 SerLeuMetGluValSerIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 585 AGCGTAGAGAAATGGGCTTAACATGGCCAGCTCTTCCACATCTCCGACGACGAC 644
QY 201 HisCysAlaGlnThrHisProAlaAspPheAsnArgArgThrAsnGluProGln 220
Db 645 CACTGTGCCAAACACGCCAGAGCTGACTTCAACAGAGACGACCAATAGCCGCGAG 704
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlnAspSerProSerHisIleLys 240
Db 705 AACGTGAAGTCTCTCCACAGAACTCCGAGTGAGAGAGACTCTCCCTCCACATCAAA 764
QY 241 ArgThrSerHisGluSerAla 247
Db 765 CGCACATCCCATGAGAGTGCA 785

RESULT 3
US-10-614-990-1
; Sequence 1, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: P108P2
; CURRENT APPLICATION NUMBER: US/10/614,990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840,989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1283
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (45)..(788)
; OTHER INFORMATION:
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (857)..(857)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1254)..(1254)
; OTHER INFORMATION: n is equal to a, t, c, or g.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1279)..(1279)
; OTHER INFORMATION: n is equal to a, t, c, or g.
US-10-614-990-1

Alignment Scores:
Pred. No. 1 7e-165 Length: 1283
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 18 Gaps: 0

US-09-705-500a-3 (1-247) x US-10-614-990-1 (1-1283)
QY 1 MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db 45 ATGTGCAAAATCGACAGTCTTGCTGGTGTGATGAGTCTTCTGGAACCATGAG 104
QY 21 AlAGlGlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 105 GCGAGACGAATGACTCTGTGAGCCCGACGAAATCCCGAGTGGCGGCCCAAACTCAGCT 164

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QY 41 GluValAlaArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 165 GAAGGTGTTCTTGCTTCCACAGAGTCTTCAACAGTGGCTTCCGAGGCTTTTGACATGCTG 224
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 225 GMAATCTCACCTGTGACACAGATGGATGTATGATCATCTTAATCTTCTTGTACAGC 284
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 285 GCTGCTAAATTTGACACTCAGAGAAAGCATCTTCTCAAGAGACCTTAATAATGATCGCC 344
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 345 AACGGGTGACCTCCAGAGTCTTCTCGCATGTGGAGTGTCTCATCTTCCAAAGGATG 404
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 405 ATTGCTGAGTGACAGAAAGATGTGTACAGCAAGCTGATGTGTGACATCGCAAGCGG 464
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 465 AACCTGAGGCATCAGAGAGTGTGTCCAGCTGCCCATCTTCCAAAGATATCAT 524
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db 525 AAGACACTTGTCGAAAGCTCTGTGAATGTATGAAGACAGACAGCAGACATCAGAGAC 584
QY 181 SerLeuMetGluValSerIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 585 AGCGTAGAGGAAATGGGCTTAACATGGCCAGCTCTTCCACATCTCCGACAGAC 644
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgGlnAsnGluProGln 220
Db 645 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGAGACGACCAATGAGCCGCGAG 704
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGlnAspSerProSerHisIleLys 240
Db 705 AAGCTGAAGTCTTCTCAGGAACTCCGAGGTGAGAGGACTCTCCCTCCACATCAAA 764
QY 241 ArgThrSerHisGluSerAla 247
Db 765 CGCACATCCCATGAGAGTGCA 785

RESULT 4
US-10-641-643-1502
; Sequence 1502, Application US/10641643
; Publication No. US20040077003A1
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; Susan G. Stuart
; Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
; GENE EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; INCYTE PHARMACEUTICALS, INC.
; ADDRESS: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643
; FILING DATE: 14-Aug-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:

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APPLICATION NUMBER: <Unknown>  
Filing Date: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1502:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3757 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9975297  
SEQUENCE DESCRIPTION: SEQ ID NO: 1502 :  
US-10-641-643-1502  
  
Alignment Scores:  
Pred. No.: 1,04e-164 Length: 3757  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-705-500a-3 (1-247) x US-10-641-643-1502 (1-3757)  
  
QY 1 MetLeuGlnaSenSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
DB 160 ATGCTCCAAAACACAGAGAGCTTCGTGCTGATCATGCTCTTCCAAACCCATGAG 219  
QY 21 AlaGluGlnaSenSerAlaSerProArgLysSerArgValAlaAlaGlnaSenSerAla 40  
DB 220 GCGGAGAGAAATATCTCTGAGACCCAGAAATCCCGAGTGGCGCTCAAAACTAGCT 279  
QY 41 GluValValArgCysLeuSenSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
DB 280 GAAGTGGTTCGTGCTCCAAAGTGTCTTACAGTGGCTGGCGGAGCTTTTGATGCCG 339  
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
DB 340 GAAATCTCCACCTGTCGACAGATGGAGATGATGACATCTGTAATCTCTTGTGACG 399  
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
DB 400 GCTGCTAAATTTGACACTCGGAGAAAGCATTCGTCAAGAGAGCTTAAATGCAATCGCC 459  
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
DB 460 AACGGGGTCACTCCCAAGGCTCTTCCTCGCATTCGAGGTGCTCCACTTCCAAAGGATG 519  
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 520 ATTGCTAGAGTGAGAGAGAGTGTCTACAGCACTGATGTCGAGCATCGCAAGCGG 579  
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
DB 580 AACCTCGAACCACATCATGTAGGTGCTCCAGCTGCCAATCATCTTCCAAAGATCATAT 639  
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
DB 640 AACAGATTGTCGAGACCTGCTGGAATGTGATGAGACACATCGACATCGCAAGAGC 699  
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
DB 700 AGCTGTATGAGAAATTTGGGCTTAACATGGCCAGCTCTTCCACTTCGACAGACAGAC 759  
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220

DB 760 CACTGTGCCAAACACACCCAGAGTGACTTCAACAGAGACGCAATGAGCCGAG 819  
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluLysSerProSerHisIleLys 240  
DB 820 AAGCTGAAGTCTCTCTCCAGAACTTCGAGGTGAGAGAGACTCTCCCTCCACATCAA 879  
QY 241 ArgThrSerHisGluSerAla 247  
DB 880 CGCACATCCCATGAGAGTGCA 900  
  
RESULT 5  
US-10-044-090-638  
Sequence 638, Application US/10044090  
Publication No. US20020137081A1  
GENERAL INFORMATION:  
APPLICANT: Olga Bandman  
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
FILE REFERENCE: PA-0028 US  
CURRENT APPLICATION NUMBER: US/10/044,090  
NUMBER OF SEQ ID NOS: 850  
SOFTWARE: PERL Program  
SEQ ID NO 638  
LENGTH: 3765  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: Incyte ID No. US20020137081A1 331181.1  
LOCATION: 2378, 3184, 3187, 3194  
OTHER INFORMATION: a, t, c, g, or other  
US-10-044-090-638  
  
Alignment Scores:  
Pred. No.: 1,04e-164 Length: 3765  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: Gaps: 0  
US-09-705-500a-3 (1-247) x US-10-044-090-638 (1-3765)  
  
QY 1 MetLeuGlnaSenSerAlaValLeuLeuValLeuValIleSerAlaSerAlaThrHisGlu 20  
DB 174 ATGCTCCAAAACACAGAGAGCTTCGTGCTGATCATGCTCTTCCAAACCCATGAG 223  
QY 21 AlaGluGlnaSenSerAlaSerProArgLysSerArgValAlaAlaGlnaSenSerAla 40  
DB 234 GCGGAGAGAAATGATCTCTGAGACCCAGAAATCCCGAGTGGCGCTCAAAACTAGCT 293  
QY 41 GluValValArgCysLeuSenSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
DB 294 GAAGTGGTTCGTGCTCCAAAGTGTCTTACAGTGGCTGGCGGAGCTTTTGATGCCG 353  
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
DB 354 GAAATCTCCACCTGTCGACAGATGGAGATGATGACATCTGTAATCTCTTGTGACG 413  
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
DB 414 GCTGCTAAATTTGACACTCGGAGAAAGCATTCGTCAAGAGAGCTTAAATGCAATCGCC 473  
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
DB 474 AACGGGGTCACTCCCAAGGCTCTTCTCGCATTCGAGGTGCTCCACTTCCAAAGGATG 533  
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 534 ATTGCTAGAGTGAGAGAGTGTCTACAGCACTGATGTCGAGCATCGCAAGCGG 593  
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160



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Db      594 AACCTGAAACCCATCTGAGTGCCTCCAGCTGCCAATCACTTCCCAACGATCTCTAT 653
Qy      161 AasnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      654 AACGACCTTCCGAAACCCCTGCTGGAATGTGATGAAAGACACAGTCAACATCAAGAGAC 713
Qy      181 SerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      714 AGCCTGATGAGAAAATTGGGCTTAACATGCGCAGCCTCTCCACATCTCCGACAGACAGAC 773
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db      774 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGAGACGACCAATGACCGCAG 833
Qy      221 LysLeuValValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
Db      834 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGTGAGAGAGACTCTCTCCCTCCACATCAAA 893
Qy      241 ArgThrSerHisGluSerAla 247
Db      894 CGCACATCCCATGAGAGTGCA 914

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## RESULT 6

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US-10-198-846-13651
; Sequence 13651, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 13651
; LENGTH: 3897
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 3878, 3879, 3880, 3881, 3882, 3883, 3884, 3885, 3886, 3887,
; LOCATION: 3888, 3889, 3890, 3891, 3892, 3893, 3894, 3895, 3896, 3897
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-13651

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## Alignment Scores:

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Pred. No.: 1.1e-164 Length: 3897
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 14 Gaps: 0

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US-09-705-500a-3 (1-247) x US-10-198-846-13651 (1-3897)

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Qy      1 MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db      285 ATGCTCCAAACATCAGACAGTCTCTCTGCTGTGATCATGTCTTTCACACCATGAG 344
Qy      21 AlaGluGlnAsnAspSerValSerProArgLysSerArgAlaAlaGlnAsnSerAla 40
Db      345 GCGAGACGAAATGACTCTGTAGCCCAAGAAATCCGAGTGGCGCTCAAACTCAGCT 404
Qy      41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60

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Db      405 GAGTGTCTTCTGCTTCAACAAGTCTCTTACAGTGGCTGGGGCTTTTGATGCTGT 464
Qy      61 GluAsnSerThrCysAspThrAspGluMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      465 GAAAACTCCACTGTGACACAGATGGGATGTATGACATCTGTAATCTCTTGTACAGC 524
Qy      81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100
Db      525 GCTGCTAAATTGACACTCAGAGAAAGCATTCGCAAGAGAGCTTAAATGATGCGC 584
Qy      101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      585 AACGGGTGACCTCCAAAGTCTTCTCGCCATTTGGAGGTCTCCACTTCCAAAGGATG 644
Qy      121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      645 ATTGCTGAGGTGCAGAGAGAGTGTCTACAGCAAGTGAATGTGTGACATGCGAAGCG 704
Qy      141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      705 AACCTGAAGCCATCAGTGAAGTGTCTCAGCTGCCAATCACTTCCAAACATCACTAT 764
Qy      161 AasnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      765 AACAGACTTGTCCGAAGCCTGCTGAATGTATGATGAAGACACAGTCAGCACATCAGAGAC 824
Qy      181 SerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      825 ACCCTGATGAGAAATTTGGGCTTACATGAGCCAGCTCTTCCATCTTCCAGACAGAC 884
Qy      201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProGln 220
Db      885 CACTGTGCCAAACACACCCACGAGCTGACTTCAACAGAGACGACCAATGAGCGCAG 944
Qy      221 LysLeuValValLeuLeuArgAsnLeuArgGlyGlnGluAspSerProSerHisIleLys 240
Db      945 AAGCTGAAAGTCTCTCTCAGGAACCTCCGAGTGAGAGAGACTCTCTCCCTCCACATCAAA 1004
Qy      241 ArgThrSerHisGluSerAla 247
Db      1005 CGCACATCCCATGAGAGTGCA 1025

```

## RESULT 7

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US-10-177-293-440
; Sequence 440, Application US/10177293
; Publication No. US20030124128A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavairpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Horrobagyl, Gabriel N.
; APPLICANT: Fustic, Lajos
; APPLICANT: Weric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572

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/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/306,501
/ PRIOR FILING DATE: 2001-07-18
/ PRIOR APPLICATION NUMBER: US 60/325,002
/ PRIOR FILING DATE: 2001-09-25
/ PRIOR APPLICATION NUMBER: US 60/362,585
/ PRIOR FILING DATE: 2002-03-05
/ PRIOR APPLICATION NUMBER: US 60/xxx,xxx
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 506
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 440
/ LENGTH: 3901
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-177-293-440

Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-10-177-293-440 (1-3901)

QY 1 MetLeuGlnAnsSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
DB ATGCTCCAAAACCTCAGACAGTCTTCTGCTGATCATGCTTCTCCACCCCATGTAG 344
QY 21 AlaGlnGlnAnsSerAlaSerProArgLysSerArgValAlaAlaGlnAnsSerAla 40
DB GCGGAGCAGATATCTCTGTGAGCCCGAGAAATCCCGATGGCGGCTCAAACTCATGCT 404
QY 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB GAAGTGGTGTGCTGCTCCCAACAGTCTCTACAGTGGCGGCGGCTTTGGATGCTCG 464
QY 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB GAAAACTCCACCTGTGACAGATGGAGATGTATGATCTGTAAATCTTCTGTATCAGC 524
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
DB GCTGCTAAATTTGACATCAGGAAAGCATTCGTCAAAAGAGCTTAAATGCAATCGCC 584
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB AACGGGGTCACTCCCAAGGCTTCTCCGCAATCGAGGCTCCCACTTCCAAAGGAGTG 644
QY 121 IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB ATTGCTGAGGTGACAGAGAGTCTCTACAGACGTAAATGTGTGACGATCCCAAGCGG 704
QY 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB AACCTCGAAGCCATCTCATGAGTCTGCTCCAGCTGCCAATCACTTCCCAAGATACTAT 764
QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
DB AACAGACTTTCTCCAGACCTGCTGGAATGTATGAACACAGTCCAGCAATCCAGAGAC 824
QY 181 SerLeuMetGlnLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
DB AGCTCATGAGAAATTTGGGCTTAACATGCGCAGCTCTTCACATCTCGACAGACAGAC 884
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGlnProGln 220
DB CACTGTGCCCCAACAACAACCCAGAGCTGACTTCAACAGAGAGAGCCACATATAGCCGAG 944
QY 221 LysLeuLysValLeuLeuArgLeuArgLeuArgGlyGlnGluAspSerProSerHisIleLys 240
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DB 945 AAGCTGAAAGTCTCTCAGGAACCTCCAGAGTGAGAGAGACTCTCCCTCCCATCAAA 1004
QY 241 ArgThrSerHisGluSerAla 247
DB CGCAGATCCCATGAGAGTGCA 1025

RESULT 8
US-10-465-572-17
/ Sequence 17, Application US/10465572
/ Publication No. US20030207840A1
/ GENERAL INFORMATION:
/ APPLICANT: Rigging, Gregory
/ TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
/ FILE REFERENCE: 000250.00012
/ CURRENT APPLICATION NUMBER: US/10/465,572
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US/10/201,642
/ PRIOR FILING DATE: 2002-07-24
/ PRIOR APPLICATION NUMBER: 60/307,600
/ PRIOR FILING DATE: 2001-07-26
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 3901
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-10-465-572-17

Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-10-465-572-17 (1-3901)

QY 1 MetLeuGlnAnsSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
DB ATGCTCCAAAACCTCAGACAGTCTTCTGCTGATCATGCTTCTCCACCCCATGAG 344
QY 21 AlaGlnGlnAnsSerAlaSerProArgLysSerArgValAlaAlaGlnAnsSerAla 40
DB GCGGAGCAGATATCTCTGTGAGCCCGAGAAATCCCGATGGCGGCTCAAACTCATGCT 404
QY 41 GluValValArgCysLeuAnsSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
DB GAAGTGGTGTGCTGCTCCCAACAGTCTCTACAGTGGCGGCGGCTTTGGATGCTCG 464
QY 61 GluAnsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
DB GAAAACTCCACCTGTGACAGATGGAGATGTATGATCTGTAAATCTTCTGTATCAGC 524
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
DB GCTGCTAAATTTGACATCAGGAAAGCATTCGTCAAAAGAGCTTAAATGCAATCGCC 584
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
DB AACGGGGTCACTCCCAAGGCTTCTCCGCAATCGAGGCTCCCACTTCCAAAGGAGTG 644
QY 121 IleAlaGlnValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
DB ATTGCTGAGGTGACAGAGAGTCTCTACAGACGTAAATGTGTGACGATCCCAAGCGG 704
QY 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
DB AACCTCGAAGCCATCTCATGAGTCTGCTCCAGCTGCCAATCACTTCCCAAGATACTAT 764
QY 161 AsnArgLeuValArgSerLeuLeuGlnCysAspGluAspThrValSerThrIleArgAsp 180
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Db 765 AACGAGCTTGCCGAGCCTGCTGATGTGATGAGACAGATGACATTCAGAGAC 824  
Qy 181 SerLeuMeGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
Db 825 AGCCTATGAGAAATTGGGCTTACATGGCCAGCCTCTTCCACATCTCTGACAGAC 884  
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
Db 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGCGACCAATGAGCCGCG 944  
Qy 221 LysLeuLysValIleuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
Db 945 AACCTGAAAGTCTCTCTCCAGAACCTCCGAGTGAGAGAGACTCTCTCCACATCAAA 1004  
Qy 241 ArgThrSerHisGluSerAla 247  
Db 1005 CGCACATCCCATGAGAGTGCA 1025  
RESULT 9  
US-10-159-563-292  
; Sequence 292, Application US/10159563  
; Publication No. US20040009154A1  
; GENERAL INFORMATION:  
; APPLICANT: Khan, Javed  
; APPLICANT: Ringner, Markus  
; APPLICANT: Peterson, Carsten  
; APPLICANT: Melzer, Paul  
; TITLE OF INVENTION: SELECTIONS OF GENES AND METHODS OF USING THE SAME FOR  
; FILE REFERENCE: 11613.58US11  
; CURRENT APPLICATION NUMBER: US/10/159, 563  
; CURRENT FILING DATE: 2002-12-09  
; PRIOR APPLICATION NUMBER: US 10/133, 937  
; PRIOR FILING DATE: 2002-04-25  
; NUMBER OF SEQ ID NOS: 444  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 292  
; LENGTH: 3901  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-159-563-292  
Alignment Scores:  
Pred. No.: 1,1e-164 Length: 3901  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-705-500a-3 (1-247) x US-10-159-563-292 (1-3901)  
Qy 1 MetLeuGlnAsnSerAlaValIleuLeuValIleSerAlaSerAlaThrHisGlu 20  
Db 285 ATGCTCCAAACTCAGCAGATGCTTGTGCTGTGATCATGCTCTTCTGCAACCCATGAG 344  
Qy 21 AlAGlGlnAsnAspSerValSerProArgLysSerArgValAlaIaGlnAsnSerAla 40  
Db 345 GCGGAGCAGATGACTCTGTGAGCCCGGAAATCCCGAGTGGCGCTCAAACTGAGCT 404  
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValaPheAlaCysLeu 60  
Db 405 GAGTGGTTTGTTGCTCCTCAACAGTGTCTACAGTGGCGTGGCGCTTTTGATGCTCG 464  
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
Db 465 GAAATCCCACTCGTGACAGATGGGATGTATGACATCTGTAATCTCTTGTGACAC 524  
Qy 81 AlAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
Db 525 GCTGCTAAATTGACATCTGAGGAGAAAGCATTTGCTCAAGAGAGCTTAAATGATCATGCG 584  
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120

Db 585 AACGGGGACCTCCAAAGTCTTCTCCGCACTTGAGAGTGCTCACCTTCCAAAGATG 644  
Qy 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
Db 645 ATTGCTGAGTGAGGAGAAAGTGTCTACAGCAAGCTGATGTGACATGCGCAACCG 704  
Qy 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
Db 705 AACCTGAGCCATCATCTGAGTGTCTCAGCTGCGCCATCATCTTCTCAACAGATCAT 764  
Qy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
Db 765 AACGACTTGTCCGAGAGCTGCTGAAATGTGATGAACACAGTCACACACATCAGAGAC 824  
Qy 181 SerLeuMeGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
Db 825 AGCCTATGAGAAATTGGGCTTACATGGCCAGCCTCTTCCACATCTCTGACAGAC 884  
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220  
Db 885 CACTGTGCCCAACACACCCAGAGCTGACTTCAACAGAGAGCGACCAATGAGCCGCG 944  
Qy 221 LysLeuLysValIleuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
Db 945 AACCTGAAAGTCTCTCTCCAGAACCTCCGAGTGAGAGAGACTCTCTCCACATCAAA 1004  
Qy 241 ArgThrSerHisGluSerAla 247  
Db 1005 CGCACATCCCATGAGAGTGCA 1025  
RESULT 10  
US-10-372-683-40  
; Sequence 40, Application US/10372683  
; Publication No. US20040009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRITSEN, MARY E.  
; APPLICANT: PEALE CR., FRANKLIN V.  
; APPLICANT: WU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOMA  
; FILE REFERENCE: P1928R1P1  
; CURRENT APPLICATION NUMBER: US/10/372, 683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271, 690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344, 534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 40  
; LENGTH: 3901  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-372-683-40  
Alignment Scores:  
Pred. No.: 1,1e-164 Length: 3901  
Score: 1268.00 Matches: 247  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
Gaps: 0  
US-09-705-500a-3 (1-247) x US-10-372-683-40 (1-3901)  
Qy 1 MetLeuGlnAsnSerAlaValIleuLeuValIleSerAlaSerAlaThrHisGlu 20  
Db 285 ATGCTCCAAACTCAGCAGATGCTTGTGCTGTGATCATGCTCTTCTGCAACCCATGAG 344  
Qy 21 AlAGlGlnAsnAspSerValSerProArgLysSerArgValAlaIaGlnAsnSerAla 40  
Db 345 GCGGAGCAGATGACTCTGTGAGCCCGGAAATCCCGAGTGGCGCTCAAACTGAGCT 404  
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValaPheAlaCysLeu 60

```

Db      405 GAAGTGGTTCGTCCTCAACAGTCTACAGTGGCGGGGCTTTGGATGCGG 464
Qy      61  GLAAsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAAACCTCTTGTAACAC 524
Qy      81  ALAAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db      525 GCTGCTAAATTTACACTCAGGAGAAAGCATTTGTCMAAGAGCTTAAATGTCATCGCC 584
Qy      101 ASnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      585 AAGGGGTCACCTCCAAAGGCTCTCCCGCATTCGAGGGTCCCACTTCCAAAGGATG 644
Qy      121 ILAAlaGluValGlnGlnGluGlyTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      645 ATTGCTGAGGTGACGAGAGAGTCTACAGCACTGATATGTGTGACGATCCGCAAGCG 704
Qy      141 ASnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      705 AACCTGAAAGCCACTGAGGTGCTCCAGCTGCCAATCACTTCCAAAGATCTAT 764
Qy      161 ASnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      765 AACAGACTGTCCGAAAGCTGTGAGATGTATGAAGACAGTCAAGCAATCAGAGAC 824
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      825 AGCTGATGAGAAATTTGGGCTTAATGCGCAGCTCTTCCACATCTCGACAGACAGC 884
Qy      201 HICysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db      885 CACTGTGCCCAACACACACCCAGAGTGACTTCMAAGAGAGAGCCCATATAGCCGCGAG 944
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db      945 AACCTGAAGTCTCTCTCAGGAACCTCCAGGTGAGAGAGACCTCTCCCAATCAAA 1004
Qy      241 ArgThrSerHisGluSerAla 247
Db      1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 11
US-10-240-425-1425
; Sequence 1425, Application US/10240425
; Publication No. US2004003502A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Amanda
; APPLICANT: Boland, Joseph F.
; APPLICANT: Lord, Reginald V.
; APPLICANT: Alvarez, Chris
; APPLICANT: Metzel, Jon C.
; APPLICANT: Scheit, Uwe
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
; FILE REFERENCE: 44921-5026
; CURRENT APPLICATION NUMBER: US/10/240,425
; PRIOR FILING DATE: 2002-09-30
; PRIOR APPLICATION NUMBER: PCT/US01/09847
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/193,446
; NUMBER OF SEQ ID NOS: 1588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1425
; LENGTH: 3901
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US2004003502A1 UZ5997
US-10-240-425-1425

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Alignment Scores:
Pred. No.: 1,1e-164 Length: 3901
Score: 1268.00 Matches: 247
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Db: 16 Gaps: 0

US-09-705-500A-3 (1-247) X US-10-240-425-1425 (1-3901)
Qy      1  MetLeuGlnAsnSerAlaValLeuLeuValIleSerAlaSerAlaThrHisGlu 20
Db      285 ATGCTCCAAATTCAGACAGTGTCTGTGCTGTGATCAGTGTCTTGCAACCCATGAG 344
Qy      21  ALAAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 40
Db      345 GCGAGAGAGATGATGCTGTGTGAGCCCGAGAAATCCGAGTGGCGGCTCAAACTAGCT 404
Qy      41  GLUValValArgCysLeuAsnSerAlaLeuGlnValGlyGlyValAlaPheAlaCysLeu 60
Db      405 GAAGTGTTCGTTGCTCCCAACAGTGTCTACAGTCCGCTGCGGGCTTTGTGATGCTG 464
Qy      61  GLAAsSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db      465 GAAAACTCCACCTGTGACACAGATGGATGTATGACATCTGTAAATCTTGTGATGCG 524
Qy      81  ALAAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db      525 GCTGCTAAATTTGACCTCAGGAGAAAGCATTTGTCMAAGAGCTTAAATGTCATCGCC 584
Qy      101 ASnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db      585 AAGGGGTCACCTCCAAAGTCTTCTGCAATTCGAGGTGCTCCACTTCCAAAGATG 644
Qy      121 ILAAlaGluValGlnGlnGluGlyTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db      645 ATTGCTGAGGTGACGAGAGAGTCTACAGCACTGATATGTGTGACGATCCGCAAGCG 704
Qy      141 ASnProGluAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db      705 AACCTGAAGCCACTGAGGTGCTCCAGCTGCCAATCACTTCCAAAGATCTAT 764
Qy      161 ASnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180
Db      765 AACGACTGTCCGAAAGCTGTGAGATGTATGAAGACAGTCAAGCAATCAGAGAC 824
Qy      181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db      825 AGCTGATGAGAAATTTGGGCTTAATGCGCAGCTCTTCCACATCTCGACAGACAGC 884
Qy      201 HICysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGluProGln 220
Db      885 CACTGTGCCCAACACACCCAGAGTGACTTCMAAGAGAGAGCCCATATAGCCGCGAG 944
Qy      221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240
Db      945 AAGCTGAAGTCTCTCTCAGGAACCTCCAGGTGAGAGAGACCTCTCCCAATCAAA 1004
Qy      241 ArgThrSerHisGluSerAla 247
Db      1005 CGCACATCCCATGAGAGTGCA 1025

RESULT 12
US-09-925-300-486
; Sequence 486, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Ruben,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10

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PRIOR APPLICATION NUMBER: PCT/US00/05988  
PRIOR FILING DATE: 2000-03-08  
PRIOR APPLICATION NUMBER: 60/124,270  
PRIOR FILING DATE: 1999-03-12  
NUMBER OF SEQ ID NOS: 1890  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 486  
LENGTH: 2572  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURES:  
NAME/KEY: misc feature  
LOCATION: (823)  
OTHER INFORMATION: n equals a,t,g, or c  
US-09-925-300-486

Alignment Scores:  
Pred. No.: 1,75e-162 Length: 2572  
Score: 1250.00 Matches: 246  
Percent Similarity: 99.19% Conservative: 0  
Best Local Similarity: 99.19% Mismatches: 1  
Query Match: 98.58% Indels: 1  
DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-09-925-300-486 (1-2572)

QY 1 MetLeuGlnAsnSerAlaValIleuValIleSerAlaSerAlaThrHisGlu 20  
Db 265 ATGCTCCAAACACAGAGCTTCTGGTGTGTATCAGCTTCTCAACCCATGAG 324  
QY 21 AlAGluGlnAsnSerValSerProArgLysSerArgValAlaIaGlnSerAla 40  
Db 325 GCGGAGAGATGACTCTGTGAGCCCAAGAAATCCCGAGTGGCGCTCAAACTAGCT 384  
QY 41 GluValAlaArgCysIleuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60  
Db 385 GAAGTGTGTGCTGCTCAACAGTCTCAAGTGGCTGGCGGCTTTGTATGCTCG 444  
QY 61 GlnAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
Db 445 GAATCTCCACCTGTGACACAGATGGATGTATGACATCTGTAAATCTTTGTACAC 504  
QY 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCysIleAla 100  
Db 505 GCTGCTAAATTTGACACTCAGGAGAAAGCATCTGTCAAGAGCTTAAATGCATCGCC 564  
QY 101 AsnGlyValThrSerLysValIlePheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
Db 565 AAGGGGTCCCTCCAGAGTCTTCTGGCTGAGGAGGTGCTCCACTTCCAAAGAGT 624  
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
Db 625 ATGCTGAGGTGAGAGAGAGTGTCTACAGCACTGATGTGTGCAAGCATCGCAAGCGC 684  
QY 141 AsnProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
Db 141 AACAGACTTCCGAAAGCTGCTGGAATGTGATGAAGACACAGCTCAGCAATCAGAGC 804  
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180  
Db 745 AACAGACTTCCGAAAGCTGCTGGAATGTGATGAAGACACAGCTCAGCAATCAGAGC 804  
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAs 200  
Db 805 AGCTGTGAGAGAAATTNGGGCTTAAACATGCGCACTCTTCCATCCTGAGACAGA 864  
QY 200 pHISYValAGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGluProG 220  
Db 865 CCACTGCGCCAAACACACACAGAGTGAATCTTCAACAGAGACGACCAATGAGCGCA 924  
QY 220 nLysLeuLysValIleuValArgAsnLeuArgGlyGluGluAspSerProSerHisIleL 240  
Db 925 GAAGCTGAAGTCTCTCTCAGGAACCTCCGAGGTGAGAGAGTCTCTCTCCACATCAA 984

QY 240 sArgThrSerHisGlnSerAla 247  
Db 985 ACGCAGATCCCATGAGAGTGA 1006

RESULT 13

US-09-778-320-149

/ Sequence 149, Application US/09778320  
/ Patent No. US20010034052A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Dillon, Davin C.  
/ APPLICANT: Day, Craig H.  
/ APPLICANT: Jiang, Yugui  
/ APPLICANT: Houghton, Raymond L.  
/ APPLICANT: Mitcham, Jennifer  
/ APPLICANT: Wang, Tongtong  
/ APPLICANT: McNeill, Patricia D.  
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
/ FILE REFERENCE: 210121.491C5  
/ CURRENT APPLICATION NUMBER: US/09/778,320  
/ NUMBER OF SEQ ID NOS: 301  
/ SOFTWARE: FastSeq for Windows Version 3.0  
/ SEQ ID NO 149  
/ LENGTH: 585  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: misc feature  
/ LOCATION: (1)...(585)  
/ OTHER INFORMATION: n=A,T,C or G  
US-09-778-320-149

Alignment Scores:  
Pred. No.: 2.01e-109 Length: 585  
Score: 861.00 Matches: 166  
Percent Similarity: 98.22% Conservative: 0  
Best Local Similarity: 98.22% Mismatches: 3  
Query Match: 67.90% Indels: 0  
DB: Gaps: 0

US-09-705-500a-3 (1-247) x US-09-778-320-149 (1-585)

QY 79 TyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValIleGlnSerLeuLysCys 98  
Db 6 TACANCACTGCTTAATTTGACACTNANGAAGAAACATTGCTCAAGAGCTTAAATGC 65  
QY 99 IleAlaAsnGlyValThrSerLysValIlePheLeuAlaIleArgArgCysSerThrPheGln 118  
Db 66 ATCGCAACGGGGTCACTCCCAAGTCTTCTCCCAATTCGAGGTCTCCACTTCCAA 125  
QY 119 ArgMetIleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAla 138  
Db 126 AGATGATTTGCTGAGGTGAGAGAGAGTGTACAGCAAGCTGATGTGTGAGCATGGCC 185  
QY 139 LysArgAsnProGluAlaIleThrGluValAlaGlnLeuProAsnHisPheSerAsnArg 158  
Db 186 AAGCGAAGCTTGAAGCCATCATGAGGTGTCTCAGCTGCCCAATCATCTTCCAAAGGA 245  
QY 159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178  
Db 246 TACTATAACAACCTTGTCCGAAGCTGCTGGAAGTGTGATGAAGACAGATGACAAATC 305  
QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198  
Db 306 AGAGCAAGCTGATGAGAGAAATTTGGGCTTAATGAGCGCACTCTTCCATCCTGAG 365  
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218  
Db 366 ACAGACCACTGTGCCAAACACACCCAGAGCTCACTTCAACAGAGACGACCAATGAG 425  
QY 219 ProGlnLysLeuLysValIleuValArgAsnLeuArgGlyGluGluAspSerProSerHis 238

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Db 426 CCGCAAGAGCTGAAAGTCCCTCCAGAAACCTCCGAGGAGAGAGACTCTCCCTCCAC 485
Qy 239 ILeysArghrSerHsgUserAla 247
Db 486 ATCAAAAGCAATCCCATGAGAGTGA 512

RESULT 14
US-09-910-689-149
; Sequence 149, Application US/09910689
; Patent No. US20020081609A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C6
; CURRENT APPLICATION NUMBER: US/09/910,689
; CURRENT FILING DATE: 2001-07-20
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A,T,C or G
US-09-910-689-149

Alignment Scores:
Pred. No.: 2,01e-109 Length: 585
Score: 861.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 9 Gaps: 0

US-09-705-500A-3 (1-247) x US-09-910-689-149 (1-585)
Qy 79 TySerAlaAlaIySphAspThrGlnGlyLysAlaPheValIySgIusSerLeuYsCys 98
Db 6 TACANCACTGCTAAATTGACACTNANNGAAGAAAGCAATGCTCAAGAGACTTAAATGC 65
Qy 99 ILeAlaAsnGlyValIhrSerIySValPheLeuAlaIleArgArGysSerThrPheGln 118
Db 66 ATGCCCAAGGGGTCACTCCCAAGGCTCTCCCTCCGCAATTCGAGGGTCTCCACTTCCAA 125
Qy 119 ArgMetIleAlaGluValGlnGluGluCysTyrSerIyLeuAsnValCysSerIleAla 138
Db 126 AGAGTAGTTGCTAGAGTGCGAGAGAGTCTACAGCAAGCTGAATGTGCGAGCAATCGCC 185
Qy 139 LysArgAsnProGluAlaIleThrGluValIleGlnLeuProAsnHisPheSerAsnArg 158
Db 186 AACGGAAACCTCGAAGCCATCACTGAGTGCTCCACTGCCCAATCACTTCCAAACAGA 245
Qy 159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
Db 246 TACTATAACAGACTTGTCGCAAGCTCGGATGATGAAGACACACTCGACCAAC 305
Qy 179 ArgAsnSerLeuMetGluValIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
Db 306 AGGACAGAGCTGATGAGAAATTTGGCTTACATGCGACCTCTTCCACATCTTCGAG 365
Qy 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgArgThrAsnGlu 218
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Db 366 ACAGACCACTGTGCCCCAAGACACCCAGAGTGACTTCAACAGAGACGACCAATGAG 425
Qy 219 ProGlnIySLeuYsValIleLeuArgAsnLeuArgGlyGluGluAspSerProSerHis 238
Db 426 CCGCAAGAGCTGAAAGTCCCTCCAGAAACCTCCGAGGAGAGAGACTCTCCCTCCAC 485
Qy 239 ILeysArghrSerHsgUserAla 247
Db 486 ATCAAAAGCAATCCCATGAGAGTGA 512

RESULT 15
US-10-010-742-149
; Sequence 149, Application US/10010742
; Publication No. US20020146727A1
; GENERAL INFORMATION:
; APPLICANT: Dillon, Davin C.
; APPLICANT: Day, Craig H.
; APPLICANT: Jiang, Yugu
; APPLICANT: Houghton, Raymond L.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Wang, Tonglong
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Bennington, Angela Ann
; APPLICANT: Zehnener, Barbara
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF BREAST CANCER
; FILE REFERENCE: 210121.491C7
; CURRENT APPLICATION NUMBER: US/10/010,742
; CURRENT FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 307
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 10, 30, 32, 527, 565
; OTHER INFORMATION: n = A,T,C or G
US-10-010-742-149

Alignment Scores:
Pred. No.: 2,01e-109 Length: 585
Score: 861.00 Matches: 166
Percent Similarity: 98.22% Conservative: 0
Best Local Similarity: 98.22% Mismatches: 3
Query Match: 67.90% Indels: 0
DB: 13 Gaps: 0

US-09-705-500A-3 (1-247) x US-10-010-742-149 (1-585)
Qy 79 TySerAlaAlaIySphAspThrGlnGlyLysAlaPheValIySgIusSerLeuYsCys 98
Db 6 TACANCACTGCTAAATTGACACTNANNGAAGAAAGCAATGCTCAAGAGACTTAAATGC 65
Qy 99 ILeAlaAsnGlyValIhrSerIySValPheLeuAlaIleArgArGysSerThrPheGln 118
Db 66 ATGCCCAAGGGGTCACTCCCAAGGCTCTCCCTCCGCAATTCGAGGGTCTCCACTTCCAA 125
Qy 119 ArgMetIleAlaGluValGlnGluGluCysTyrSerIyLeuAsnValCysSerIleAla 138
Db 126 AGAGTAGTTGCTAGAGTGCGAGAGAGTCTACAGCAAGCTGAATGTGCGAGCAATCGCC 185
Qy 139 LysArgAsnProGluAlaIleThrGluValIleGlnLeuProAsnHisPheSerAsnArg 158
Db 186 AACGGAAACCTCGAAGCCATCACTGAGTGCTCCACTGCCCAATCACTTCCAAACAGA 245
Qy 159 TyrTyrAsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIle 178
Db 246 TACTATAACAGACTTGTCGCAAGCTCGGATGATGAAGACACACTCGACCAATC 305
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QY 179 ArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGln 198
Db 306 AGAGACAGCCTGATGAGAAATTGGGCTTAACATGGCCAGCCTTCCACATCCTGCGAG 365
QY 199 ThrAspHisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrAsnGln 218
Db 366 ACAGACCACCTGTGCCCAACACACAGCAGCTGACTTCAACAGAGACGACCAATGAG 425
QY 219 ProGluLysLeuLysValLeuLeuArgAsnLeuArgGlyGlnGlnAspSerProSerHis 238
Db 426 CCGGAGAGCTGAAGTCTCTCTGAGAACCTCCGAGGTGAGGAGACTCTCTCTCCAC 485
QY 239 IleLysArgThrSerHisGlnSerAla 247
Db 486 ATCAAAGCACATCCCATGAGAGTGCA 512

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Search completed: November 22, 2004, 19:26:25  
 Job time : 540 secs

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QY 21 AlagluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40  
DB 345 GCGAGAGAGATATCTCTGTGAGCCCGAGAAATCCCGAGTGGCGCTCAAACTCAGCT 404  
QY 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLeu 60  
DB 405 GAAGTGGTTCGTCCTCCCAACAGTCTTACAGTCCGGCTGGCGGCTTTTGATGCTCG 464  
QY 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80  
DB 465 GAAACCTCCACCTGTGACAGATGGATGTATGACATCTGTAAATCCTTTGTACACG 524  
QY 81 AlAlaIalysPheAspThrGlnGlyLysAlaPheValLysGluSerLeuLysCysIleAla 100  
DB 525 GCTGCTAAATTTACACTCAGGAGAAAGCATTCGTCAAGAGAGCTTAAATAGCATCGCG 584  
QY 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120  
DB 585 AACGGGTGACCTCCACAGGTCTCTCCGCTCCATTCGAGGTGCTCCACTTCCAAAGAGATG 644  
QY 121 IleAlaGluValGlnGluGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140  
DB 645 ATTGCTAGGTGCGAGAGAGTCTTACAGCAAGCTGATGTGTGACGATCCGCAAGCGG 704  
QY 141 AsnProGluAlaIleThrGluValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160  
DB 705 AACCTGAACCATCACTGAGTGTGCTGACAGCTCCCAATCACTTCCAAACAGATCTAT 764  
QY 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrAlaSerThrIleArgAsp 180  
DB 765 AACGACTTGTCCGAACTGTGTGATGTATGATGAACACATCCACATCAGAGAC 824  
QY 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200  
DB 825 AGCTGTATGAGAAATATGGGCTTAACATGCGCAGCTCTTCCATCTCGACAGACAG 884  
QY 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgArgThrGlnGluProGln 220  
DB 885 CACTGTGCCCAACACACCCACAGCTGACTTCAACGAGAGAGACCAATGAGCGCAG 944  
QY 221 LysLeuLysValLeuLeuArgAsnLeuArgGlyGluGluAspSerProSerHisIleLys 240  
DB 945 AAGCTGAAGTCTCTCCAGGAACCTCCGAGGAGAGAGAGAGAGAGAGAGAGAGAGAG 1004  
QY 241 ArgThrSerHisGluSerAla 247  
DB 1005 CGCACATCCCATGAGAGTGCA 1025

## RESULT 2

US-10-956-160-4242  
; Sequence 4242, Application US/10956160  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
; FILE REFERENCE: 031896-044000 (AM101084)  
; CURRENT APPLICATION NUMBER: US/10/956,160  
; NUMBER OF SEQ ID NOS: 222274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4242  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-956-160-4242

## Alignment Scores:

Pred. No.: 1,44e-35 Length: 422  
Score: 366.00 Matches: 75  
Percent Similarity: 98.68% Conservative: 0  
Best Local Similarity: 98.68% Mismatches: 0  
Query Match: 28.86% Indels: 1

DB: 6 Gaps: 0  
US-09-705-500a-3 (1-247) x US-10-956-160-4242 (1-422)  
QY 1 MetLeuGlnAsn-SerAlaValLeuValIleSerAlaSerAlaThrHisG 20  
DB 195 ATGCTCCAAATCTCACAGAGTCTTCTGTGCTGTATGATGAGCTTCTCAACCATGA 254  
QY 20 uAlaGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAl 40  
DB 255 GCGGAGAGAGATATTTCTGTGAGCCCGAGAAATCCCGGTGGCAGCTCAGAACTCAGC 314  
QY 40 aGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLe 60  
DB 315 TGAAGTGGTTCGTCCTCCACAGTCTTGCAGAGTTCGCTGGCGGCTTTTGATGCTCG 374  
QY 60 uGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLys 75  
DB 375 GGAAGACTCCACTGTGACAGATGGATGTATGACATCTGTAA 420

## RESULT 3

US-10-956-160-214349  
; Sequence 214349, Application US/10956160  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION IN ANIMAL  
; TITLE OF INVENTION: MODELS OF INFLAMMATORY DISEASES  
; FILE REFERENCE: 031896-044000 (AM101084)  
; CURRENT APPLICATION NUMBER: US/10/956,160  
; NUMBER OF SEQ ID NOS: 222274  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 214349  
; LENGTH: 422  
; TYPE: DNA  
; ORGANISM: Canis familiaris  
US-10-956-160-214349

## Alignment Scores:

Pred. No.: 1,44e-35 Length: 422  
Score: 366.00 Matches: 75  
Percent Similarity: 98.68% Conservative: 0  
Best Local Similarity: 98.68% Mismatches: 0  
Query Match: 28.86% Indels: 1  
DB: 6 Gaps: 0

US-09-705-500a-3 (1-247) x US-10-956-160-214349 (1-422)

QY 1 MetLeuGlnAsn-SerAlaValLeuValIleSerAlaSerAlaThrHisG 20  
DB 195 ATGCTCCAAATCTCACAGAGTCTTCTGTGCTGTATGATGAGCTTCTCAACCATGA 254  
QY 20 uAlaGluGlnAsnSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAl 40  
DB 255 GCGGAGAGAGATATTTCTGTGAGCCCGAGAAATCCCGGTGGCAGCTCAGAACTCAGC 314  
QY 40 aGluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyValAlaPheAlaCysLe 60  
DB 315 TGAAGTGGTTCGTCCTCCACAGTCTTGCAGAGTTCGCTGGCGGCTTTTGATGCTCG 374  
QY 60 uGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLys 75  
DB 375 GGAAGACTCCACTGTGACAGATGGATGTATGACATCTGTAA 420

## RESULT 4

US-10-900-423-12  
; Sequence 12, Application US/10900423  
; GENERAL INFORMATION:  
; APPLICANT: GOTO, MASAAKI  
; APPLICANT: TOMOYASU, AKIHIRO  
; APPLICANT: YANO, KAZUKI  
; APPLICANT: KOBAYASHI, FUMIE

```

/ APPLICANT: NAKAGAWA, NOBUAKI
/ APPLICANT: YASUDA, HISATAKA
/ APPLICANT: YAMAGUCHI, KYOJI
/ APPLICANT: KINOSAKI, MASAHITO
/ APPLICANT: MOCHIZUKI, SHIN-ICHI
/ APPLICANT: NAKAKARUWAI, TADASHI
/ APPLICANT: MORINAGA, TOMONORI
/ APPLICANT: TSUDA, SISUKE
/ APPLICANT: HIGASHIO, KUNJI
/ TITLE OF INVENTION: NOVEL PROTEIN AND PROCESSES FOR PRODUCING THE SAME
/ FILE REFERENCE: 239674USOPCT
/ CURRENT APPLICATION NUMBER: US/10/900,423
/ PRIOR FILING DATE: 2004-07-28
/ PRIOR APPLICATION NUMBER: US/09/647,907
/ PRIOR FILING DATE: 2000-12-04
/ PRIOR APPLICATION NUMBER: PCT/JP99/01906
/ PRIOR FILING DATE: 1999-04-09
/ PRIOR APPLICATION NUMBER: JP 243355/1998
/ PRIOR FILING DATE: 1998-08-28
/ PRIOR APPLICATION NUMBER: JP 99741/1998
/ PRIOR FILING DATE: 1998-04-10
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 12
/ LENGTH: 862
/ TYPE: DNA
/ ORGANISM: Homo Sapiens
/ US-10-900-423-12

```

```

Alignment Scores:
Pred. No.: 1,236-33      Length: 862
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
                        Gaps: 4

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US-09-705-500a-3 (1-247) x US-10-900-423-12 (1-862)

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Qy 9 LeuValIleuValIleSer-----AlaSerAlaThrHisGluAla 21
Db 7 CTGGCTTGGTGTGGTGGCACCCTTGACCGCGCGGGGAGCAGCCAGCCACCAACCCACC 66
Qy 22 Gln--GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 67 GAGGGTCCCAAGACAGAGAGCTCCAGCAAGAAAGCGCGCTGTCTGCAGAAATACAGCG 126
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 127 GAGATCCAGACCTGTGTGTCACAGCTGGCGATGTGGGGTGGGCTGTGTGATGATTTTC 186
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 187 GAGAACCACTCTGTGAGATTGGGGCTTACATGAGTTTGATGACTTTTTCGCAACAC 246
Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 247 GCTGGAATAATTATATGCGCCAGGCAAGTCACTTCAAAAGACCTTGAAATGTAAAGGC 306
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 307 CACGCTCTGGGCAACAGCTTCGGCTCGCATTAAGCCGAAGTCCCGGCCCATCAGGAAAG 366
Qy 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 367 GTGTCCAGATGGCAGCGGAGATCTACCTCAACAGACAGACTGTGCGCGCTGCCAGAG 426
Qy 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160
Db 427 AATGACCCGGGTGATAGTGGAGATGATCCATTTCAGAGACTGTGCTGCACGAACCTTAC 486
Qy 161 AsnArgLeuValArgSerLeuLeuGluCysAspGluAspThrValSerThrIleArgAsp 180

```

```

Db 487 GTGACCTCTGTGAAGTCTGTGATCCTGTGGGGAGAGAGTGAAGAGGACCATCACCCAC 546
Qy 181 SerLeuMetGluLysIleGlyProAsnMetAlaSerLeuPheHisIleLeuGlnThrAsp 200
Db 547 AGCTGTGAGGTTCAGATGTGACAGAGACTGGGGAAGCCCTGTCTCATCTTG-----AGC 600
Qy 201 HisCysAlaGlnThrHisProArgAlaAspPheAsnArgA-GArgThrAsnGluProGln 220
Db 601 TTCTGCACCTGGGC-CATCCAGAAAGCTCCACAGCGCGCCCCCGACGCCACGCCAGCT 659
Qy 221 LysLeuLysValIleLeuArgAsn--LeuArgGlyGlnGluAspSerPro 236
Db 660 GGACAGAACCAAGCTCTCCAGGGCCACACAGGGGGAAGCAGACATCACT 710

```

RESULT 5  
US-10-956-157-1106  
Sequence 1106, Application US/10956157

```

/ GENERAL INFORMATION:
/ APPLICANT: Wyeth
/ APPLICANT: Mounts, William
/ TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
/ TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
/ FILE REFERENCE: 031896-043000 (AW 101081)
/ CURRENT APPLICATION NUMBER: US/10/956,157
/ PRIOR FILING DATE: 2004-10-04
/ NUMBER OF SEQ ID NOS: 319805
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1106
/ LENGTH: 2380
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ US-10-956-157-1106

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Alignment Scores:
Pred. No.: 5,286-33      Length: 2380
Score: 354.00           Matches: 82
Percent Similarity: 52.32% Conservative: 42
Best Local Similarity: 34.60% Mismatches: 102
Query Match: 27.92%      Indels: 12
                        Gaps: 4

```

US-09-705-500a-3 (1-247) x US-10-956-157-1106 (1-2380)

```

Qy 9 LeuValIleuValIleSer-----AlaSerAlaThrHisGluAla 21
Db 168 CTGGCTTGGTGTGGTGGCACCCTTGACCGCGCGGGGACCGAGCCACCAACCCACC 227
Qy 22 Gln--GlnAsnAspSerValSerProArgLysSerArgValAlaAlaGlnAsnSerAla 40
Db 228 GAGGGTCCCAAGAGAGAGCTCCAGCAAGAAAGCGCGCTGTCTGCAGAAATACAGCG 287
Qy 41 GluValValArgCysLeuAsnSerAlaLeuGlnValGlyCysGlyAlaPheAlaCysLeu 60
Db 288 GAGATCCAGACCTGTGTGTCACAGCTGGCGATGTGGGGTGGGCTGTGTGATGATTTTC 347
Qy 61 GluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSerPheLeuTyrSer 80
Db 348 GAGAACCACTCTGTGAGATTGGGGCTTACATGAGTTTGATGACTTTTTCGCAACAC 407
Qy 81 AlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGlnSerLeuLysCysIleAla 100
Db 408 GCTGGAATAATTATATGCGCCAGGCAAGTCACTTCAAAAGACCTTGAAATGTAAAGGC 467
Qy 101 AsnGlyValThrSerLysValPheLeuAlaIleArgArgCysSerThrPheGlnArgMet 120
Db 468 CACGCTCTGGGCAACAGCTTCGGCTCGCATTAAGCCGAAGTCCCGGCCCATCAGGAAATG 527
Qy 121 IleAlaGluValGlnGlnGluCysTyrSerLysLeuAsnValCysSerIleAlaLysArg 140
Db 528 GTGTCCAGATGGCAGCGGAGATCTACCTCAACAGACAGACTGTGCTGCACGAACCTTAC 587
Qy 141 AsnProGlnAlaIleThrGlnValValGlnLeuProAsnHisPheSerAsnArgTyrTyr 160

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Alignment scores:	0.24	Length:	2025
Pred. No.:	93.50	Matches:	47
Score:	40.28†	Conservative:	38
Percent Similarity:	40.28†	Mismatches:	86
Best Local Similarity:	22.27†	Indels:	40
Query Match:	7.37†	Gaps:	9
DB:	8		

US-09-705-500A-3 (1-247) x US-60-615-573-13086 (1-2025)

QY	14	SezAlSezAlathriISgluaIagIugIaInaEnaEsSer-ValSezProArGlySserAr	33
		: :::	: :::
Db	746	AGrATCAcAGrTACrTCAcAGcATTGAcCAAArTCAAAcCTrTCAcCAcAArTTAAcAGA	805
QY	33	gValaIa-----AlaGInaSenSerIaGlUaIValaIaGcYsLeuAnSe	48
		::: :::	: :::
Db	806	AGcTATCAcATGcCTTCAAAcCAAGAAArTATrTCAcAArTAgTCAArTGTAAAAAcAG	865
QY	48	rAlaLeaGInaIValGlyCySglYalAlaPheAlaCySLeuGInaSenSerThrCySAsPThrAs	68
		: :::	: :::
Db	866	A-----CTTGAArTGTCArTAATGTATACGA	892
QY	68	pGImeTYrAsPIeCySlySerPheIeu-----TySerAlaIaIySPheAsPTh	86
		::: :::	: :::
Db	893	TCcAAcACAGGrTAgCTCAcAGAAAcATrTAArTATrTACAcCGCTAAAAAcCGAGAGAc	952
QY	86	rGInGlyIySaIaPheValIyGLeuSerIeuIyScylAlaInGly-----	102
		::: :::	: :::
Db	953	TCcAAATGA-----ATAcAAAAAcCGAcATGArTTrTAArTATrTGAAGrTGTACTGc	1006
QY	103	-----ValThSeIySaIPheIeUaIaIeArGArCy	114
		: :::	: :::
Db	1007	TCcAGATATrTCTTcGAAAAATCTrAAATAGAcAGArTATAcAGcATTACAAAAATGc	1066
QY	114	sSerThrPheGInaIyMeCilEaIaGlUaIaGInaIuCyTyISeIySleu-----	132

```

Db      1067 TAAGAATGACTTAAAGACCTGATTAAGAAAGAAATTACAGAACTGCATACACATTAACCTTAATACA 1126
OY      133  -AanValCyseSerIleAlaIysArgAenProGluAlaIleThrGluValValGlnLeuPr 152
Db      1127 AATGTTAATATCCATGTGTAAAAA---CCATCTAGATTCGAAACCTAATAGTCTGCAG 1183
OY      152 caAnHisIlePheSerAsnArgTyr-----TyrAsnArgLeuValArgSerLeuGluCy 170
Db      1184 ACGAAATATGCAAAACCAATATATATACCGCTAAATAATGAAGCACATATATGTTTGAAAA 1243
OY      170 sAspGluAspThrValSerThrIleArgAspSerLeu-----MetGluIysIleGlyPr 188
Db      1244 TACAAACCTCAGTAAATGACAGTACAGAGAGATGCTTACGTAGAGTAAATGCAATTCAAC 1303
OY      188 caAnMetAlaSerLeuPheHisIleLeuGln 198
Db      1304 AGAGGTTACAAAAGCTATTATATACTTCAA 1334

RESULT 7
US-60-788-64      ; Sequence 64, Application US/60620788
GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Sellman, Bret R.
APPLICANT: Baker, Steve M.
TITLE OF INVENTION: Immunogenic Compositions of Staphylococcus epidermidis Antigens
FILE REFERENCE: Awt101548 L
CURRENT APPLICATION NUMBER: US/60/620,788
CURRENT FILING DATE: 2004-10-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64
LENGTH: 30612
TYPE: DNA
ORGANISM: Staphylococcus epidermidis
US-60-620-788-64

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[illegible]

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Db      9225 TAAGATGACTTAAGTGTATTAAGAGATTACAGATCGATACATTAATCTTTATCA 9284
QY      133 -AsnValCysSerIleAlaLysArgAsnProGluAlaIleThrGluValAlaGlnLeuP 152
Db      9285 AAATGTTAAATACCATGTGTAATAAAA---CCATCTAGATTCAAAACATTAAGTCTGCAAG 9341
QY      152 AsnHisPheSerAspArgTyr-----TyrAsnArgLeuValArgSerLeuGluGly 170
Db      9342 ACCAAATATGCAAAACCAATATTAATACCGCTTAATAATGAACCAATATATGTTCTGAAA 9401
QY      170 sAspGluAspThrValSerThrIleArgAspSerLeu-----MetGluLysIleGlyP 188
Db      9402 TACAAACCTCACTGTAATGACAGTAAAGATGCTTTACGTAGATTAATGCAATTCACAC 9461
QY      188 cAsnMetAlaSerLeuPheHisIleLeuGln 198
Db      9462 AGAGTTACAAAAGCTATTATATACTTCAA 9492

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## RESULT 8

```

US-10-968-812-1
; Sequence 1, Application US/10968812
; GENERAL INFORMATION:
; APPLICANT: Meyers, Rachel A.
; APPLICANT: Curtis, Rory A. J.
; APPLICANT: Glucksmann, Maria Alexandra
; APPLICANT: Bandaru, Rajasekhar
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: NOVEL HUMAN GENES AND METHODS OF USE THEREOF
; FILE REFERENCE: 10448-19501
; CURRENT APPLICATION NUMBER: US/10/968, 812
; CURRENT FILING DATE: 2004-10-19
; PRIOR APPLICATION NUMBER: US/10/176,306
; PRIOR FILING DATE: 2002-06-20
; PRIOR APPLICATION NUMBER: 10/001,137
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: PCT/US01/45291
; PRIOR FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/248,362
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248,331
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/248,365
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: 60/250,077
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,327
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 60/250,176
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: 10/023,617
; PRIOR FILING DATE: 2001-12-18
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 3134
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (113)...(2131)
US-10-968-812-1

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## Alignment Scores:

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Pred. No.: 3.25 Length: 3134
Score: 86.50 Matches: 55
Percent Similarity: 37.02% Conservative: 42
Best Local Similarity: 20.99% Mismatches: 102
Query Match: 6.82% Indels: 63
DB: 6 Gaps: 13

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US-09-705-500a-3 (1-247) X US-10-968-812-1 (1-3134)

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QY      15 AlaSerAlaThrHisGluAlaGluGlnAsnAspSerValSerProAlaGlySer----- 32
Db      89 GCCTCTCAACCCACGCGCGGAGCATGACAGAAAAGACATTAAGAGAGTCCACCG 148
QY      33 -----ArgValAlaAlaGlnAsnSerAlaGluValAlaArg----- 44
Db      149 GAATGCACCGGAAATATGAGAGGGGAGCGCGCGCCCGCAAGTGGCGGCACAGACA 208
QY      45 Cys-----LeuAsnSerAlaLeuGlnValGlyCysGlyAla 56
Db      209 TGCCCCACCCCTCGGAAATACAGCAAGGTCAAGCTTCCATGAACCTGGC----- 259
QY      57 PheAlaCysLeuGluAsnSerThrCysAspThrAspGlyMetTyrAspIleCysLysSer 76
Db      260 -----CTGCTAGAGTGAAGGGCGGCTGCAGCGAAGTGAAGTCTGAGAAATGC----- 307
QY      77 PheLeuTyrSerAlaAlaLysPheAspThrGlnGlyLysAlaPheValLysGluSerLeu 96
Db      308 -----ATCCAGTCTTCGATTCACTGCGACGCTGCGACAGAGACACATG 355
QY      97 LysCysIleAlaAsnGlyValThrSerLysValPhe-----LeuAlaIleArg 112
Db      356 CTCAACATGCTGCTGCGCATGACAGCTGGGTGCTGCCCTCCCGACCTGGCTGCCGC 415
QY      113 ArgCysSerThrPheGlnArgMetIleAlaGluValGlnGluGlyCysTyrSerLysLeu 132
Db      416 CTGCTGACCTCATACACAGAGCCACAGGGGACACCCAGAG-----CTGAGACGGCTG 469
QY      133 AsnValCysSerIleAlaLys-----ArgAsnProGluAlaIleThrGluVal 148
Db      470 CAGATCTCACTGCTGATGACTGCTGATGCGACACCTGAGTGATGATCACCAGAT 529
QY      149 ValGlnLeuProAsnHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuLeu 168
Db      530 CCCCAGCTA---GAAGAAGTCAATAGTGTCTTCTGGCGCACCGTGGCCGGAG----- 580
QY      169 GluCysAspGluAspThrValSerThrIleArgAspSer-----LeuMetGluLysIle 186
Db      581 -----GGCAACTCAGCCACAGAGAGACTGGAGACTTCTGCACTCTGAGCCCTGT 634
QY      187 GlyPro-----AsnMetAla 191
Db      635 GGCCCTGGCCCCCACTCCCAATGACAGCCAGCCCTGGGCAAAAGCGCAAGTGTCC 694
QY      192 SerLeuPheHisIleLeuGlnThrAspHisCysAlaGlnThrHisProArgAlaAspPhe 211
Db      695 TTGCTTTTCAGCACTTGAGACGGGGAGGAGTGGCTGACACTCACTCACTGAGATTTC 754
QY      212 AsnArgArgArgThrAsnGluProGlnLysLeuLys-----ValLeuLeuArgAsnLeu 229
Db      755 CGGTCTTCAGGCTATGACCCCGAGACTGTGGAGCTGAGCTGTTTGCAGAGGCTCAGTA 814
QY      230 ArgGly 231
Db      815 CGAGGC 820

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## RESULT 9

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US-60-615-573-12667
; Sequence 12667, Application US/60615573
; GENERAL INFORMATION:
; APPLICANT: Wyeeth
; APPLICANT: Mounts, William M.
; APPLICANT: Murphy, Ellen
; APPLICANT: Olmsted, Stephen
; TITLE OF INVENTION: PROBE ARRAYS FOR DETECTING MULTIPLE STRAINS OF DIFFERENT SPECIES
; FILE REFERENCE: 031896-084099 (AM 101724)
; CURRENT APPLICATION NUMBER: US/60/615,573
; CURRENT FILING DATE: 2004-10-05
; NUMBER OF SEQ ID NOS: 18598
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12667
; LENGTH: 1965

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; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
US-60-615-573-12667

Alignment Scores:
Pred. No.: 2.17 Length: 1965
Score: 85.50 Matches: 42
Percent Similarity: 38.41% Conservative: 21
Best Local Similarity: 25.61% Mismatches: 70
Query Match: 6.74% Indels: 31
DB: 8 Gaps: 6

US-09-705-500a-3 (1-247) x US-60-615-573-12667 (1-1965)

QY 35 ALAAlGLIAsnSerIaGIuValArgCYsLeuAsnSerAlaLeuGluValGIcys 54
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 67 AGTGCAGAAATCTGTACTGAAATTTATTACTTGAAGTCATCTTAAGATTACCTAA 126
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 55 GLIAlaPheAlaCYsLeuGluAsnSerThrCYsAspThrAspGlyMetTyr----- 71
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 127 GGGACT-----GACATTTTGTAGTGAACCTTCATGCTGAATACGAATCTTTC 174
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 72 -----AspIleCYsIys 75
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 175 CAACATGTTTAAAGAAACGATCTGAAATGCGCTAAATTAATATATCTTCAAA 234
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 76 SerPheLeuTyrSerAlaAlaIysPheAspThrGlnGlyLysAlaPheVal---LysGlu 94
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 235 GATTAATTAATCCAGCAAGAAATCAACGACTTAGCAGCATTTGATACATCCGAGAGA 294
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 95 SerLeuLysCYsIleAlaAsnGlyValThrSerLysValPheLeuAlaIleArgArgCYs 114
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 295 AAACATAAATTAAGTTAAATTAATTCGATTCATCGAACAATTAAATTTGGTATATT 354
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 115 SerThrPheGlnArgMetIleAlaGluValGlnGluCYsTyrSerLysLeuAsnVal 134
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 355 ACAACATTAAAGCATTAAT---GATTTAATACATATTGCCATCAAAAATACACCT 411
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 135 CYsSerIleAlaIysArgAsnProGlu-----AlaIleThrGluValAlaGln 150
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DB 412 TCAAAATTAACGAACCATTAACCTGAACATACGTTATATTAATGAAGCTACTTAC 471
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 151 LeuProAsnHisPheSerAsnArg-----TyrTyrAsnArgLeuValArgSerLeuLys 168
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 472 AAGAGCAATGAATTTCAATTAATAAAGCCTTATTATGAACATTAAGTAAACCAATTATT 531
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 169 GluCYsAspGlu 172
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DB 532 GAATTGACAA 543

RESULT 10
US-10-746-294A-95/c
; Sequence 95, Application US/10746294A
; GENERAL INFORMATION:
; APPLICANT: Bush, David F.
; APPLICANT: Roundley, Steven D.
; APPLICANT: Wiesend, Roger C.
; TITLE OF INVENTION: Plant Polymorphic Markers and Uses Thereof
; FILE REFERENCE: 38-10(15493)E
; CURRENT APPLICATION NUMBER: US/10/746,294A
; PRIOR FILING DATE: 2003-12-29
; PRIOR APPLICATION NUMBER: US 09/692,412
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: US 09/534,859
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 09/803,736
; PRIOR FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 124
; SEQ ID NO 95
; LENGTH: 129516
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-10-746-294A-95

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Alignment Scores:
Pred. No.: 1.15e+03 Length: 129516
Score: 85.00 Matches: 48
Percent Similarity: 39.30% Conservative: 31
Best Local Similarity: 23.88% Mismatches: 57
Query Match: 6.70% Indels: 65
DB: 6 Gaps: 11

US-09-705-500a-3 (1-247) x US-10-746-294A-95 (1-129516)

QY 62 AsnSerThrCYsAspThrAspGlyMetTyrAspIleCYsLysSerPheLeuTyrSerAla 81
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DB 44853 AACAGCACT-----AACATCAACCAAGCTGACCTCCATGTTCCAG 44815
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 82 AlaLysPheAspThrGlnGlyLysAlaPheValLysLeuSerLeuLys----- 97
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44814 CCAATCTTCAACAGGTTAGCTGTTCTTCTTGAAGCTCCGCTTGCACCTTTGATGA 44755
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 98 CysIle-----AlaAsnGlyValThrSerLysValPheLeuAlaIle--- 111
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44754 TGTGTGGCTCTATCAAAACTGCTCGCATGTCAATATGATCTTCTTGGCTTGAAGC 44695
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 -----ArgArgCYsSerThrPheGlnArg-----MetIleAlaGluValGln 125
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44694 AGCAGAAAGCTTCAAACTTGTCAAACTAAGCCACACCTGTAAATGCTTTAGCGTCCA 44635
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 126 Glu-----GluCYs-----TyrSerLysLeuAsn 133
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DB 44634 GAGTGGCTCATATAAGCTCGTGTCTCTTAATTCCTAGATGATCTCAAAAGTCAAT 44575
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QY 134 ValCYsSerIleAlaIysArgAsnProGluAlaIleThrGluValAlaGln---LeuProAs 153
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44574 GTATGCCCATTAAGAGAGTCCGGGGGTCAAGAAACAGGCTGATGATTTGCAAGCTCAAAA 44515
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QY 153 nHisPheSerAsnArgTyrTyrAsnArgLeuValArgSerLeuGluCYsAspGluAs 173
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44514 TAGCTTAGCTCGTTCGTTCTTCAAGCAAG----- 44487
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 173 pThrValSerThrIleArgAspSerLeuMetGluLysIleGlyProAsnMetAlaSerIle 193
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DB 44486 -----AGACCTCTCAAACTCAACCAAACTGGTGCACAGCTACCAACTCT 44443
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 193 u-----PheHisIleLeuGlnThrAspHisCYsAlaGlnThrHis---ProArgAl 209
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 44442 CAGAGACCATTTCAAGATACCGGCGCATACAGCTTTCTACATCTATCTTCCCAAGT 44383
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 209 aAspPheAsnArgArgArgThrAsnGluProGlnLysLeuLysValLeuLeuArgAsnLe 229
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DB 44382 GGAGTTCAT-----CTCAATGTATTTCTTGAAAATCT 44350
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QY 229 u 229
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DB 44349 T 44349

RESULT 11
US-60-613-292-289
; Sequence 289, Application US/60613292
; GENERAL INFORMATION:
; APPLICANT: Gene Logic, Inc
; APPLICANT: Higgs, Brandon
; APPLICANT: ELASHOFF, Michael
; APPLICANT: MENDRICK, Donna L.
; APPLICANT: PORTER, Mark W.
; APPLICANT: CASTLE, Arthur L.
; APPLICANT: JOHNSON, Kory R.
; TITLE OF INVENTION: MOLECULAR TOXICITY MODELS FROM ISOLATED HEPATOCYTES
; FILE REFERENCE: 044921-5135-PR
; CURRENT APPLICATION NUMBER: US/60/613,292
; PRIOR FILING DATE: 2004-09-28
; NUMBER OF SEQ ID NOS: 1300
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 289

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QY		5	SerAlaValIleuLeuValIeu---ValIIeSerAlaSerAlaThr-----	18
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QY		19	HISGLUAlaGUlInHnaSPSeValSerProArgLysSerArgValAlaIlaGlInsn	38
Db		139	AATACTGCAAAACCMAAATCAAGAACAATCCAAAAATTTCACAGACAGCACTTACAAAT	198
QY		39	SerAlaGUlValValArgCysLeuASenSerAlaLeuGlInValGIlyCysGIyAlaPheAla	58
Db		199	AATACTGAA-----AATCAAGATGCCACAGCATATACA	231
QY		59	CysLeuGlInuAsnSerThrCysAspThr----AspGIyMetTyrrAspIIeCysLysSer	76
Db		232	ACAGATCAAATATATATATGATGAAGAAAGATACGATCGCTCATATGAACTT-----CCA	285
QY		77	PheLeuTYseRialalalySphEaSPThnGIcLYLySaIaPheValIlysGIserLeu	96
Db		286	ATTCTTTATGTAACTGCTGCGTAGATGATCAAGAAAT--ATTATTTAAAGATGCTGTG	342
QY		97	Lys-----	97
Db		343	GAAAGATGCTAAACCCCCTTGACAGAAAGCAACCGGTGAAATTCCTGGGTACCAACAT	402
QY		98	-----CysIIeaIaEngIyValThrSerLysValPheLeuAlaIIeaArgArCys	114
Db		403	TATAGAACTTCTGTGATGACGGAATTAATACTATTATTAT-----CGTAAATAT	453
QY		115	SetThrPheGIlnArgMetIIeaIGluValIGInGIuGIuCysTyrrSerLysLeuAsnVal	134
Db		454	AGCACATGCACAAATCAACTATAGTTGTAATAATCAACAAACATATATATACAAATTAAGTT	513
QY		135	CysSerIIleaIalySrGaSnProGIuaIIaIIeThnGIuValValGIInLeuProASnhIs	154
Db		514	GTTGAACAAACCAATCAATCAAAATTAAGATGAAGTAAAGGAAAGAACAA-----AAICAA	567
QY		155	PheSerAsnArgTyrrTrasnArgLeuValArgSerIeuDeuGIuCysaspGIuAspThr	174
Db		568	GCAATTACTTCAAGTAAACAATTAACAACAAT--ACCAAAAACGAGAAAGCGAAGACACA	624
QY		175	ValSerThrlleaArgSpSerIeuMetGIuLysIIeGIyProASnMetalSerIeuPhe	194
Db		625	-----AAAAACAATAAGAAAGATTAAGAYGAGAAAGAAATCTTAACACAMWAAAAACA-----	675
QY		195	HISIIleuGlInhrAspHisCysAlaGIInThrHisproArgIIaSPPhenAsnArgX	214
Db		676	-----CCAAAGAAAGACMAAAGAAAGAA	699
QY		215	ArgThrAsnGIuProGIuLys	221
Db		700	GACAMWAAAAACYCCRAAGAA	720



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: Sequence 2559, Application US/60622712
: GENERAL INFORMATION:
: APPLICANT: Klaenhammer, Todd
: APPLICANT: Russell, William
: APPLICANT: Alterman, Eric
: TITLE OF INVENTION: LACTOBACILLUS ACIDOPHILUS NUCLEIC ACIDS AND USES THEREOF
: FILE REFERENCE: 5051-604PR10
: CURRENT APPLICATION NUMBER: US/60/622,712
: CURRENT FILING DATE: 2004-10-27
: NUMBER OF SEQ ID NOS: 2559
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 2559
: LENGTH: 1993570
: TYPE: DNA
: ORGANISM: Lactobacillus acidophilus
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (61464)..(61464)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (62139)..(62139)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (416372)..(416372)
: OTHER INFORMATION: n is a, c, g, or t
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: NAME/KEY: misc feature
: LOCATION: (1630403)..(1630403)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1631417)..(1631417)
: OTHER INFORMATION: n is a, c, g, or t
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1631599)..(1631599)
: OTHER INFORMATION: n is a, c, g, or t
US-60-622-712-2559

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

CM protein - protein search, using sw model

Run on: November 22, 2004, 17:49:27 ; Search time 27 Seconds

(without alignments)  
606.687 Million cell updates/sec

Title: US-09-705-500A-3

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Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents AA:\*  
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4: /cgn2\_6/ptodata/1/1aa/6S\_COMB.pep:\*  
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6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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1	1268	100.0	247	US-08-208-005C-2	Sequence 2, Appl1
2	1268	100.0	247	US-09-038-597A-2	Sequence 2, Appl1
3	1268	100.0	247	US-08-460-529B-10	Sequence 10, Appl1
4	1268	100.0	247	US-08-431-117A-2	Sequence 2, Appl1
5	1268	100.0	247	US-09-361-736B-10	Sequence 10, Appl1
6	660.5	52.1	204	US-08-208-005C-5	Sequence 5, Appl1
7	660.5	52.1	204	US-08-038-597A-5	Sequence 5, Appl1
8	628	49.5	170	US-08-460-529B-9	Sequence 9, Appl1
9	628	49.5	170	US-09-361-736B-9	Sequence 9, Appl1
10	354.5	28.0	296	US-08-831-132-14	Sequence 14, Appl1
11	354.5	28.0	296	US-09-416-150-14	Sequence 14, Appl1
12	354	27.9	302	US-08-831-132-2	Sequence 2, Appl1
13	354	27.9	302	US-09-416-150-2	Sequence 2, Appl1
14	354	27.9	302	US-09-193-881-23	Sequence 23, Appl1
15	354	27.9	302	US-09-361-736B-12	Sequence 12, Appl1
16	351.5	27.7	251	US-09-361-736B-2	Sequence 2, Appl1
17	333.5	26.3	251	US-08-460-529B-2	Sequence 2, Appl1
18	91	7.1	901	US-09-828-062-8	Sequence 8, Appl1
19	89.5	7.1	10182	US-09-134-001C-3159	Sequence 3159, Ap
20	86	6.8	500	US-09-198-452A-289	Sequence 289, App
21	85.5	6.7	311	US-08-710-279-2460	Sequence 2460, Ap
22	85.5	6.7	656	US-09-134-001C-4332	Sequence 4332, Ap
23	83.5	6.6	290	US-09-655-908-6	Sequence 6, Appl1
24	83.5	6.6	290	US-09-655-908-8	Sequence 8, Appl1
25	83.5	6.6	1027	US-09-762-724-6	Sequence 6, Appl1
26	83.5	6.6	1029	US-09-762-724-6	Sequence 6, Appl1
27	83	6.5	319	US-09-710-279-792	Sequence 792, App

28	83	6.5	319	4	US-09-710-279-2008	Sequence 2008, Ap
29	83	6.5	398	4	US-09-710-279-44	Sequence 44, Appl
30	83	6.5	417	4	US-09-710-279-1498	Sequence 1498, Ap
31	83	6.5	417	3	US-09-134-001C-3810	Sequence 3810, Ap
32	82	6.5	362	3	US-09-134-001C-4670	Sequence 4670, Ap
33	81	6.4	680	3	US-09-298-924-4	Sequence 4, Appl1
34	81	6.4	720	2	US-08-840-236-1	Sequence 1, Appl1
35	81	6.4	720	2	US-08-505-448A-1	Sequence 1, Appl1
36	79.5	6.3	609	4	US-09-538-092-711	Sequence 711, App
37	79.5	6.3	708	1	US-08-145-681-4	Sequence 4, Appl1
38	79.5	6.3	708	2	US-08-453-703-4	Sequence 4, Appl1
39	79.5	6.3	708	2	US-08-456-106-4	Sequence 4, Appl1
40	79.5	6.3	708	3	US-08-456-108-4	Sequence 4, Appl1
41	79.5	6.3	708	3	US-09-265-577-4	Sequence 4, Appl1
42	79.5	6.3	708	4	US-09-633-739-4	Sequence 4, Appl1
43	79	6.2	264	4	US-09-134-000C-5831	Sequence 5831, Ap
44	78.5	6.2	1288	4	US-09-546-934-4	Sequence 4, Appl1
45	78	6.2	315	3	US-09-184-964-4	Sequence 4, Appl1

ALIGNMENTS

RESULT 1  
US-08-208-005C-2  
; Sequence 2, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Copulescles of Stannius Protein, Stannocalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/208.005C  
; FILING DATE: 8 MARCH 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO. 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-208-005C-2  
Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MCONSAYLVLVVISASATHEQNDVSFRKSRVAQSAWVSCINSLQVGQAFQCL 60  
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Db 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFQRM 120  
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Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDDTVSTIRD 180  
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Db 241 RTSHESA 247

RESULT 2  
US-09-038-597A-2  
; Sequence 2, Application US/09038597A  
; Patent No. 5877290  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpules of Stannius Protein,  
; TITLE OF INVENTION: Stannicalcin  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/038,597A  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8-MARCH-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: FERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-78  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-09-038-597A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1,6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
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Db 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFQRM 120  
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Db 121 IAEVQECYSKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLLCEDDTVSTIRD 180  
QY 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLPHILOTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3  
US-08-460-529B-10  
; Sequence 10, Application US/08460529B  
; Patent No. 5994103  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human stannicalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/460,529B  
; FILING DATE: June 2, 1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/13206  
; FILING DATE: 10 NOV 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PFI43)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
US-08-460-529B-10

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1,6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
Db 1 MLQNSAVLLVIVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGCAFACL 60  
QY 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFQRM 120  
Db 61 ENSTCTDGMWDICKSFLYSAAKFDIOGKAFVKSILKCIANGVTSKVFLAIRCSTFQRM 120  
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Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLSLECEDTIVSTIRD 180  
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Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVKYLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4  
US-08-431-117A-2  
; Sequence 2, Application US/08431117A  
; Patent No. 5994301  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannicalcain  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/431,117A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/208,005  
; FILING DATE: 8 MARCH 1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PERRARO, GREGORY D.  
; REGISTRATION NUMBER: 36,134  
; REFERENCE/DOCKET NUMBER: 325800-296  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1700  
; TELEFAX: 201-994-1744  
; INFORMATION FOR SRO ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-08-431-117A-2

Query Match 100.0%; Score 1268; DB 2; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MLQNSAVLLVLYISASATHEABONDVSPPKSRVAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTGMWDICGSFLYSAAKFDTGKAFVKSLSKCIANGVTSKVFLAIRCSTFORM 120  
Db 61 ENSTCDTGMWDICGSFLYSAAKFDTGKAFVKSLSKCIANGVTSKVFLAIRCSTFORM 120  
QY 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLSLECEDTIVSTIRD 180  
Db 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLSLECEDTIVSTIRD 180  
QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVKYLRLNLGGEEDSPSHIK 240

Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVKYLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 5  
US-09-361-736B-10  
; Sequence 10, Application US/09361736B  
; Patent No. 6613877  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Human Stannicalcain-Alpha  
; FILE REFERENCE: PFI43PDI  
; CURRENT APPLICATION NUMBER: US/09/361,736B  
; PRIOR FILING DATE: 1999-07-28  
; PRIOR APPLICATION NUMBER: 08/460,529  
; PRIOR FILING DATE: 1995-06-02  
; PRIOR APPLICATION NUMBER: PCT/ US94/13206  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 10  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: human  
; US-09-361-736B-10

Query Match 100.0%; Score 1268; DB 4; Length 247;  
Best Local Similarity 100.0%; Pred. No. 1.6e-136;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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QY 61 ENSTCDTGMWDICGSFLYSAAKFDTGKAFVKSLSKCIANGVTSKVFLAIRCSTFORM 120  
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QY 121 IAEVQECYCKLVNCSIAKRNPEALTEVQLPNHSNRYNRLVRSLSLECEDTIVSTIRD 180  
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QY 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVKYLRLNLGGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLFPHILQTDHCAQTHPRADFNRRRTNEPOKLVKYLRLNLGGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247  
RESULT 6  
US-08-208-005C-5  
; Sequence 5, Application US/08208005C  
; Patent No. 5837498  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Corpuscles of Stannius Protein, Stannicalcain  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; ADDRESSEE: CECCHI, STEWART & OLSTEIN  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE





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CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
City: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/831,132
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: SawiSlak, Deborah A.
REGISTRATION NUMBER: 37,438
REFERENCE/DOCKET NUMBER: 96-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6678
TELEFAX: 206-442-6672
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 302 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-831-132-2

Query Match          27.9%  Score 354; DB 3; Length 302;
Best Local Similarity 32.4%  Pred. No. 6,9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4

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Db 12 LVLVLTATPDPAKGATDATNPPEGDPDRSSQCGRLSLQNTAEIQHCLVNAAGDVCGVGECE 71

QY 61 ENSTCPTDGMNDICKSPFIYSAKPEPTDGKAFVSESLKCIANGTSTVPLAIRPCSTFFQRM 120
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Db 72 ENNSCIRGLHICMTFPLHNGKFPDAQGSFTKDALKCKAHALRHPGCTSRKCPAIREM 131

QY 121 IAEVGECECKSNVCSIAKRNPEAITEVQLFNHFSNRYNRLVRSILDECEDEPTVSTIRD 180
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 132 VSGIQRECTLKIDLCAPAQENTRIVIEHIFKDLILHEPVVDLVNLLITGGEVKEAITH 191

QY 181 SLMEKIGPMNASLFILO-THCAQTHPRADFNRRFRNEQKL----- 222
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 192 SVQVQCEQNMWGSILCSILSFCTSAIQKPEPTAPERPQVDRTKLRAHGEAGHLLPEPSS 251

QY 223 KYVLRLRLGGEEDSPSH 238
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Db 252 RETGRGAKGERSKSH 267

RESULT 13
US-09-416-150-2
Sequence 2, Application US/09416150
Patent No. 6171822
GENERAL INFORMATION:
APPLICANT: Kuestner, Rolf E.
Conklin, Darrell C.
Ick, Si
Buddle, Michele
Downey, William
TITLE OF INVENTION: STANNIOCALCIN-2
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
City: Seattle
STATE: WA

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; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/416,150
; FILING DATE: 11-Oct-1999
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/831,132
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A.
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 96-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6678
; TELEFAX: 206-442-6672
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 302 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-416-150-2

Query Match      27.9%; Score 354; DB 3; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRVAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAATPDPAAGTDTATPPGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALKCKAHALRHFGCISRKCPAIREM 131
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITTEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQIQRECYLKHDLCAAAQENTRVIVEMHFKDILLHEPYVDLVNLLTGCBEVKEAITH 191
QY 181 SLMEKIGPMNASLPHILQ-TDHCAGTHPRADFNRRRTNEPOKL----- 222
DB 192 SVQVQCEQNWGSLCSILSFTCSAIQKPEPTAPPERQPOVDRTKLSRAHGHGHHLPBPS 251
QY 223 KVLRLNLRGEEDSPSH 238
DB 252 RETGRGAKGERGSKSH 267

RESULT 14
US-09-193-881-23
; Sequence 23, Application US/09193881A
; Patent No. 6538119
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Paula N. Friedman
; APPLICANT: Edward N. Granados
; APPLICANT: Michael R. Klases
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for Detecting Diseases of the
; FILE REFERENCE: 6248 US P1
; CURRENT APPLICATION NUMBER: US/09/193,881A
; CURRENT FILING DATE: 1998-11-18
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; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 302
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-193-881-23

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Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRVAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAATPDPAAGTDTATPPGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALKCKAHALRHFGCISRKCPAIREM 131
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RESULT 15
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; Sequence 12, Application US/09361736B
; Patent No. 6613877
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stem/localcin-Alpha
; FILE REFERENCE: PFI43PDI
; CURRENT APPLICATION NUMBER: US/09/361,736B
; CURRENT FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 12
; LENGTH: 302
; TYPE: PRT
; ORGANISM: human
US-09-361-736B-12

Query Match      27.9%; Score 354; DB 4; Length 302;
Best Local Similarity 32.4%; Pred. No. 6.9e-32;
Matches 83; Conservative 45; Mismatches 102; Indels 26; Gaps 4;

QY 9 LVLVIS-----ASATHEAE-QNDSVSPKRSRVAQNSAEVAVRCINSALOYGCGAFACL 60
DB 12 LALVLAATPDPAAGTDTATPPGPDSSQKGRSLQNTAEIQHCLVNAAGVGGVFECE 71
QY 61 ENSTCDTDMYDICKSFLYSAAKFDTOGKAFVKESLKCIANGVTSKYFLAIRCSTFGQM 120
DB 72 ENNSCEIRGLHGICMTPLHNAKGFDAQGSFIDALKCKAHALRHFGCISRKCPAIREM 131
QY 121 IAEVQEECYSKLVNCSIAKRNPEAITTEVQLPNHFSNRYYNRLVRSLLCEDEDTVSTIRD 180
DB 132 VSQIQRECYLKHDLCAAAQENTRVIVEMHFKDILLHEPYVDLVNLLTGCBEVKEAITH 191
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Db 252 RETGRGAKGERGSKSH 267

Search completed: November 22, 2004, 18:05:57  
Job time : 30 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2004, 17:56:22 ; Search time 83 Seconds

(Without alignments)  
1053.850 Million cell updates/sec

Title: US-09-705-500A-3

Perfect score: 1268  
Sequence: 1 MGNLSAVLLVLTIVISASATHE.....NLNGEDSPSHIKTSHESA 247

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Gap 10.0 , Gapext 0.5

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 1570615

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*

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- 2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	1268	100.0	247	9	US-09-840-989A-2	Sequence 2, Appl1
2	1268	100.0	247	9	US-09-361-736-10	Sequence 10, Appl1
3	1268	100.0	247	13	US-10-116-051-2	Sequence 2, Appl1
4	1268	100.0	247	14	US-10-117-293-441	Sequence 441, Appl1
5	1268	100.0	247	14	US-10-418-226-10	Sequence 10, Appl1
6	1268	100.0	247	14	US-10-465-572-18	Sequence 18, Appl1
7	1268	100.0	247	15	US-10-372-683-41	Sequence 41, Appl1
8	1268	100.0	247	17	US-10-614-990-2	Sequence 2, Appl1
9	937	73.9	276	9	US-09-925-300-1426	Sequence 1426, Appl1
10	662.5	52.2	256	9	US-09-840-989A-3	Sequence 3, Appl1
11	660.5	52.2	256	17	US-10-614-990-3	Sequence 10, Appl1
12	660.5	52.2	204	13	US-10-116-051-10	Sequence 9, Appl1
13	628	49.5	170	9	US-09-361-736-9	Sequence 9, Appl1

14	628	49.5	170	14	US-10-418-226-9	Sequence 9, Appl1
15	358	28.2	70	9	US-09-864-761-37770	Sequence 37770, A
16	354	27.9	302	9	US-09-193-881-23	Sequence 23, Appl1
17	354	27.9	302	14	US-10-177-293-43	Sequence 443, Appl1
18	354	27.9	302	14	US-10-338-395-23	Sequence 23, Appl1
19	354	27.9	302	14	US-10-418-226-12	Sequence 12, Appl1
20	354	27.9	302	14	US-10-364-889-4	Sequence 4, Appl1
21	354	27.9	302	14	US-10-295-027-100	Sequence 100, Appl1
22	354	27.9	302	15	US-10-173-999-80	Sequence 80, Appl1
23	354	27.9	302	15	US-10-058-370A-22	Sequence 22, Appl1
24	351.5	27.7	251	14	US-10-418-226-2	Sequence 2, Appl1
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26	303	23.9	118	13	US-10-116-051-9	Sequence 9, Appl1
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29	92	7.3	1010	17	US-10-425-115-312927	Sequence 312927, A
30	91	7.2	901	10	US-09-828-062-8	Sequence 8, Appl1
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33	90	7.1	281	11	US-09-973-278-172	Sequence 172, Appl1
34	90	7.1	281	11	US-09-973-278-277	Sequence 277, Appl1
35	90	7.1	331	15	US-10-264-049-2324	Sequence 2324, Appl1
36	89.5	7.1	622	16	US-10-437-963-161551	Sequence 161551, A
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40	89	7.0	431	17	US-10-425-115-285165	Sequence 285165, A
41	86	6.8	401	15	US-10-425-114-63193	Sequence 63193, A
42	86	6.8	470	15	US-10-282-122A-54827	Sequence 54827, A
43	86	6.8	500	15	US-10-289-762-299	Sequence 299, Appl1
44	86	6.8	529	17	US-10-425-115-320053	Sequence 320053, A
45	85.5	6.7	564	15	US-10-424-599-272057	Sequence 272057, A

#### ALIGNMENTS

RESULT 1  
US-09-840-989A-2  
; Sequence 2, Application US/09840989A  
; Patent No. US20020042372A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stemlocalcin Polynucleotides, Polypeptides, and Methods Based The  
; FILE REFERENCE: PFI0892  
; CURRENT FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-840-989A-2

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9.9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	ENSTDPTGMYDICKSFLYSAAKPTQGAAYKSKLKIANGVTSKVLAIARRCSTFORM	120
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QY	121	INVEVEGCKSKNVGSIKRNPEAITTEVVOLENHSNNYRLVSLIECEDPTVSTTRD	180

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QY 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 2  
US-09-361-736-10  
; Sequence 10, Application US/09361736  
; Patent No. US20020102634A1  
; GENERAL INFORMATION:  
; APPLICANT: OLSEN, ET AL.  
; TITLE OF INVENTION: Human Stannocalcin-alpha  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
; STREET: 6 BECKER FARM ROAD  
; CITY: ROSELAND  
; STATE: NEW JERSEY  
; COUNTRY: USA  
; ZIP: 07068  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5 INCH DISKETTE  
; COMPUTER: IBM PS/2  
; OPERATING SYSTEM: MS-DOS  
; SOFTWARE: WORD PERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/361,736  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/460,529  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: MULLINS, J.G.  
; REGISTRATION NUMBER: 33,073  
; REFERENCE/DOCKET NUMBER: 325800-334 (PF143)  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-994-1744  
; TELEFAX: 201-994-1700  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 247 AMINO ACIDS  
; TYPE: AMINO ACID  
; STRANDEDNESS:  
; TOPOLOGY: LINEAR  
; MOLECULE TYPE: PROTEIN  
; US-09-361-736-10

Query Match 100.0%; Score 1268; DB 9; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVGGCAFACL 60  
Db 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLAIRRCSIFQRM 120  
Db 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLAIRRCSIFQRM 120  
QY 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
Db 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
QY 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240

Db 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 3  
US-10-116-051-2  
; Sequence 2, Application US/10116051  
; Publication No. US20020146791A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: CORPUSCLES OF STANNIUS PROTEIN, STANNICALCIN  
; FILE REFERENCE: PF108PDI01  
; CURRENT APPLICATION NUMBER: US/10/116,051  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: 09/312,610  
; PRIOR FILING DATE: 1999-05-17  
; PRIOR APPLICATION NUMBER: 08/431,117  
; PRIOR FILING DATE: 1995-04-28  
; PRIOR APPLICATION NUMBER: 08/208,005  
; PRIOR FILING DATE: 1994-03-08  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO: 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-116-051-2

Query Match 100.0%; Score 1268; DB 13; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9, 9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVGGCAFACL 60  
Db 1 MLQNSAVLLVIVISASATHEAEQNDVSYPKRSRYAAQNSAEVVRCLNSALQVGGCAFACL 60  
QY 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLAIRRCSIFQRM 120  
Db 61 ENSTCDTDGMYDICKSPFLYSAAKFTDQKAFVKSLLKCIANGVTSKVFLLAIRRCSIFQRM 120  
QY 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
Db 121 IAEVQECYKLVNCSIAKRNPEAITVEVOLPNHFSNRYNRLVRSLLCEDEPTVSTIRD 180  
QY 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
Db 181 SLMEKIGPNMASLFPHIQTQDHCAQTHPRADFNRRRTNEPQKLVLLRNLRGEEDSPSHIX 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 4  
US-10-177-293-441  
; Sequence 441, Application US/10177293  
; Publication No. US20030124128A1  
; GENERAL INFORMATION:  
; APPLICANT: Lillie, James  
; APPLICANT: Glatc, Karen  
; APPLICANT: Zhao, Xumei  
; APPLICANT: Gannavarpu, Manjula  
; APPLICANT: Kamatkar, Shubhangi  
; APPLICANT: Mettem, Maureen  
; APPLICANT: Myer, Vic  
; APPLICANT: Wang, Youzhen  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Hoersch, Sebastian  
; APPLICANT: Monahan, John  
; APPLICANT: Meyers, Rachel E.

```

; APPLICANT: Bast Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Pusztai, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sahin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; FILE REFERENCE: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MFI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 441
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-441

Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 5
US-10-418-226-10
; Sequence 10; Application US/10418226
; Publication No. US20030181663A1
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: Human Stemlocalcin-Alpha
; FILE REFERENCE: PFI43PID2
; CURRENT APPLICATION NUMBER: US/10/418,226
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 09/361,736
; PRIOR FILING DATE: 1999-07-28
; PRIOR APPLICATION NUMBER: 08/460,529
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: PCT/ US94/13206
; PRIOR FILING DATE: 1994-11-30
; NUMBER OF SEQ ID NOS: 12
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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: human
US-10-418-226-10

Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
QY 241 RTSHESA 247
DB 241 RTSHESA 247

RESULT 6
US-10-465-572-18
; Sequence 18; Application US/10465572
; Publication No. US20030207840A1
; GENERAL INFORMATION:
; APPLICANT: Riggs, Gregory
; APPLICANT: Lal, Anita
; TITLE OF INVENTION: GENES INDUCED BY HYPOXIA
; FILE REFERENCE: 000250.00012
; CURRENT APPLICATION NUMBER: US/10/465,572
; CURRENT FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US/10/201,642
; PRIOR FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: 60/307,600
; PRIOR FILING DATE: 2001-07-26
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-465-572-18

Query Match      100.0%; Score 1268; DB 14; Length 247;
Best Local Similarity 100.0%; Pred. No. 9,9e-121;
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
DB 1 MLQNSAVLLVVISASATHEAEQNDVSPPKSRVAAQNSAEVVRCLNSALQVCGAFACL 60
QY 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
DB 61 ENSTCDTGMWDICSFYSAKFDTGKAFVKSILKCIANGVTSKVFIAIRRCSTFORM 120
QY 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
DB 121 IAEVQEECYSKLVNCSIAKRNPEALTEVQLPNHFSNRYNRLVRSLLCEDEDTVSTIRD 180
QY 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
DB 181 SLMEKIGPNNASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKYLRLRGEEDSPSHIK 240
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Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240  
QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 7  
US-10-372-683-41  
; Sequence 41, Application US/10372683  
; Publication No. US2004009171A1  
; GENERAL INFORMATION:  
; APPLICANT: GERRIESEN, MARY E.  
; APPLICANT: PEARL JR., FRANKLIN V.  
; APPLICANT: KU, THOMAS D.  
; TITLE OF INVENTION: METHODS FOR THE TREATMENT OF CARCINOVA  
; FILE REFERENCE: P19281P1  
; CURRENT APPLICATION NUMBER: US/10/372,683  
; CURRENT FILING DATE: 2003-02-21  
; PRIOR APPLICATION NUMBER: US 10/271,690  
; PRIOR FILING DATE: 2002-10-16  
; PRIOR APPLICATION NUMBER: US 60/344,534  
; PRIOR FILING DATE: 2001-10-18  
; NUMBER OF SEQ ID NOS: 49  
; SEQ ID NO 41  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-372-683-41

Query Match 100.0%; Score 1268; DB 15; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
Db 1 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTDGMWDICKSFLYSAKFDTOGKAFVHESLKCIANGVTSKVFLAIRRCSFTQRM 120  
Db 61 ENSTCDTDGMWDICKSFLYSAKFDTOGKAFVHESLKCIANGVTSKVFLAIRRCSFTQRM 120

QY 121 IAAVQEECYSKLVNCSIAKRNPEAITVEVOLPHNFSRNYNRLVRSLLCEDDVTSTIRD 180  
Db 121 IAAVQEECYSKLVNCSIAKRNPEAITVEVOLPHNFSRNYNRLVRSLLCEDDVTSTIRD 180

QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240

QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 8  
US-10-614-990-2  
; Sequence 2, Application US/10614990  
; Publication No. US20040198658A1  
; GENERAL INFORMATION:  
; APPLICANT: Olsen et al.  
; TITLE OF INVENTION: Stannocalcin Polynucleotides, Polypeptides, and Methods Based TH  
; FILE REFERENCE: P1108P2  
; CURRENT APPLICATION NUMBER: US/10/614,990  
; CURRENT FILING DATE: 2003-07-09  
; PRIOR APPLICATION NUMBER: US/09/840,989A  
; PRIOR FILING DATE: 2001-04-25  
; PRIOR APPLICATION NUMBER: PCT/US00/29432  
; PRIOR FILING DATE: 2000-10-26  
; PRIOR APPLICATION NUMBER: US 60/161,740  
; PRIOR FILING DATE: 1999-10-27  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2  
; LENGTH: 247  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-614-990-2

Query Match 100.0%; Score 1268; DB 17; Length 247;  
Best Local Similarity 100.0%; Pred. No. 9,9e-121;  
Matches 247; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
Db 1 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60

QY 61 ENSTCDTDGMWDICKSFLYSAKFDTOGKAFVHESLKCIANGVTSKVFLAIRRCSFTQRM 120  
Db 61 ENSTCDTDGMWDICKSFLYSAKFDTOGKAFVHESLKCIANGVTSKVFLAIRRCSFTQRM 120

QY 121 IAAVQEECYSKLVNCSIAKRNPEAITVEVOLPHNFSRNYNRLVRSLLCEDDVTSTIRD 180  
Db 121 IAAVQEECYSKLVNCSIAKRNPEAITVEVOLPHNFSRNYNRLVRSLLCEDDVTSTIRD 180

QY 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240  
Db 181 SLMEKIGPNMASLPHILQTDHCAQTHPRADFNRRRTNEPQKLKVLRLNGEEDSPSHIK 240

QY 241 RTSHESA 247  
Db 241 RTSHESA 247

RESULT 9  
US-09-925-300-1426  
; Sequence 1426, Application US/09925300  
; Patent No. US20020151681A1  
; GENERAL INFORMATION:  
; APPLICANT: Craig Rosen.  
; APPLICANT: Steve Ruben.  
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
; FILE REFERENCE: PA101  
; CURRENT APPLICATION NUMBER: US/09/925,300  
; CURRENT FILING DATE: 2001-08-10  
; PRIOR APPLICATION NUMBER: PCT/US00/059988  
; PRIOR FILING DATE: 2000-03-08  
; PRIOR APPLICATION NUMBER: 60/124,270  
; PRIOR FILING DATE: 1999-03-12  
; NUMBER OF SEQ ID NOS: 1890  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1426  
; LENGTH: 276  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURES:  
; NAME/KEY: SITE  
; LOCATION: (43)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (273)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (275)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-925-300-1426

Query Match 73.9%; Score 937; DB 9; Length 276;  
Best Local Similarity 99.5%; Pred. No. 6,6e-87;  
Matches 185; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 60  
Db 89 MLQNSAVILVIVISASATHEAEQNDVSPPKSRVAQNSAEVVRCLNSALQVCGGAFACL 148

QY 61 ENSTCDTDGMWDICKSFLYSAKFDTOGKAFVHESLKCIANGVTSKVFLAIRRCSFTQRM 120

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Db      149 ENSCTDDGMDICKSLFYSAKAFDTQGAFAVESLSKCIANGVTSKYFLAIRRCSFTQRM 208
Qy      121 IAEVQECYSKLVNCSIAKRNPEATEVQLPNHFSNRYNRLVRSLLCEDTSTIRD 180
Db      209 IAEVQECYSKLVNCSIAKRNPEATEVQLPNHFSNRYNRLVRSLLCEDTSTIRD 268
Qy      181 SLMEXI 186
Db      269 SLMEXI 274
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## RESULT 10

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US-09-840-989A-3
; Sequence 3, Application US/09840989A
; Patent No. US20020042372A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanninocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/09/840, 989A
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-09-840-989A-3
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Query Match      52.2%; Score 662.5; DB 9; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
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Qy      11 LVISASATHEAEQNDVSPPKSRVAQAQNSAEVVCUNSLALQVCGAFACLENSTCDTDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRARFSSNSPSDVARCLNGALAVGCGTACLENSTCDTDGM 70
Qy      71 YDICKSFLYSAKAFDTQGAFAVESLSKCIANGVTSKYFLAIRRCSFTQRMIAEVOECYS 130
Db      71 HDICQLFHTAATFTQGTFTVKSLSKCIANGVTSKYFQTRRCGVGFQRMISEVOECYS 130
Qy      131 KLVNCSIAKRNPEATEVQLPNHFSNRYNRLVRSLLCEDTSTIRDSLMKIGPNM 190
Db      131 RLDICGVARSNPEALGEVYQVPAHPRNRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
Qy      191 ASLFHILQTDHCAQTHPRADFN---RRRTNEPQKLKVLRLNLRGEEDESPSHI 239
Db      191 ETLFOLLQNKHCPOGSGNCPNSAPAGRWPMGSPSPFKI-QPSMRGRD--PTHL 241
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## RESULT 11

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US-10-614-990-3
; Sequence 3, Application US/10614990
; Publication No. US20040198658A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: Stanninocalcin Polynucleotides, Polypeptides, and Methods Based Th
; FILE REFERENCE: PFI08P2
; CURRENT APPLICATION NUMBER: US/10/614, 990
; CURRENT FILING DATE: 2003-07-09
; PRIOR APPLICATION NUMBER: US/09/840, 989A
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: PCT/US00/29432
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: US 60/161,740
; PRIOR FILING DATE: 1999-10-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-614-990-3
```

```
Query Match      52.2%; Score 662.5; DB 17; Length 256;
Best Local Similarity 53.4%; Pred. No. 6e-59;
Matches 125; Conservative 46; Mismatches 54; Indels 9; Gaps 4;
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Qy      11 LVISASATHEAEQNDVSPPKSRVAQAQNSAEVVCUNSLALQVCGAFACLENSTCDTDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRARFSSNSPSDVARCLNGALAVGCGTACLENSTCDTDGM 70
Qy      71 YDICKSFLYSAKAFDTQGAFAVESLSKCIANGVTSKYFLAIRRCSFTQRMIAEVOECYS 130
Db      71 HDICQLFHTAATFTQGTFTVKSLSKCIANGVTSKYFQTRRCGVGFQRMISEVOECYS 130
Qy      131 KLVNCSIAKRNPEATEVQLPNHFSNRYNRLVRSLLCEDTSTIRDSLMKIGPNM 190
Db      131 RLDICGVARSNPEALGEVYQVPAHPRNRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
Qy      191 ASLFHILQTDHCAQTHPRADFN---RRRTNEPQKLKVLRLNLRGEEDESPSHI 239
Db      191 ETLFOLLQNKHCPOGSGNCPNSAPAGRWPMGSPSPFKI-QPSMRGRD--PTHL 241
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## RESULT 12

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US-10-116-051-10
; Sequence 10, Application US/10116051
; Publication No. US20020146791A1
; GENERAL INFORMATION:
; APPLICANT: Olsen et al.
; TITLE OF INVENTION: COSPUSCLES OF STANNIUS PROTEIN, STANNILOCALCIN
; FILE REFERENCE: PFI08PDI01
; CURRENT APPLICATION NUMBER: US/10/116,051
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 09/312,610
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 08/431,117
; PRIOR FILING DATE: 1995-04-28
; PRIOR APPLICATION NUMBER: 08/208,005
; PRIOR FILING DATE: 1994-03-08
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Oncorhynchus kisutch
US-10-116-051-10
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Query Match      52.1%; Score 660.5; DB 13; Length 204;
Best Local Similarity 60.8%; Pred. No. 7e-59;
Matches 118; Conservative 38; Mismatches 37; Indels 1; Gaps 1;
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Qy      11 LVISASATHEAEQNDVSPPKSRVAQAQNSAEVVCUNSLALQVCGAFACLENSTCDTDGM 70
Db      12 LVIGTAATFTDTPDEA-SPRARFSSNSPSDVARCLNGALAVGCGTACLENSTCDTDGM 70
Qy      71 YDICKSFLYSAKAFDTQGAFAVESLSKCIANGVTSKYFLAIRRCSFTQRMIAEVOECYS 130
Db      71 HDICQLFHTAATFTQGTFTVKSLSKCIANGVTSKYFQTRRCGVGFQRMISEVOECYS 130
Qy      131 KLVNCSIAKRNPEATEVQLPNHFSNRYNRLVRSLLCEDTSTIRDSLMKIGPNM 190
Db      131 RLDICGVARSNPEALGEVYQVPAHPRNRYSTLLQSLACDEETVAVVRAGLVARLGPDM 190
Qy      191 ASLFHILQTDHCAQ 204
Db      191 ETLFOLLQNKHCPO 204
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## RESULT 13

```

      / PRIOR FILING DATE: 1995-06-02
      / PRIOR APPLICATION NUMBER: PCT/ US94/13206
      / PRIOR FILING DATE: 1994-11-30
      / NUMBER OF SEQ ID NOS: 12
      / SOFTWARE: PatentIn version 3.1
      / SEQ ID NO 9
      / LENGTH: 170
      / TYPE: PRT
      / ORGANISM: Anguilla australis
      / US-10-418-226-9

Query Match      49.5%; Score 628; DB 14; Length 170;
Best Local Similarity 66.5%; Pred.No.1,1e-55;
Matches 113; Conservative 30; Mismatches 27; Indels 0; Gaps 0;

QY      28 SPKSHVAQNSAEVVRCLNSALQVCGAFACLENSTCDTGMVYDICKSFLVSAKFPDQ 87
DB      1 SPTTAFSSSSSDVARCLNGALQVCGSAFACLDNSTCTDMHICSFLLGAAKFPDQ 60
QY      88 GRAFVFESIKCIANGVTSKVFPLAIRRCSTFQOMIAVEQBECKSKNVGSIARNEATE 147
DB      61 GKTFVESHKCIANGTTSKVFPLIRCCSFQMISEVEBECKSKLDLSVAQNSPEANGE 120
QY      148 VQGLPHFENRYNNRLVRSILCEDEPYTIRDSIMEXPMASIFLFL 197
DB      121 VQGVPEQFENRYTSTLQSLTCDDEDTYEQVAGVSRLEPMGVFLQL 170

RESULT 15
US-09-864-761-37770
/ Sequence 37770, Application US/09864761
/ Patent No. US20020048763A1
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aemica-X-1
/ CURRENT APPLICATION NUMBER: US/09/864,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687

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; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 37770
; LENGTH: 70
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC012119.1
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.1
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.7
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.2
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 2.7
; OTHER INFORMATION: SWISSPROT HIT: P52823, EVALUE 3.00e-35
; OTHER INFORMATION: EST_HUMAN HIT: AW954342.1, EVALUE 3.00e-34
US-09-864-761-37770
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Query Match          28.2%; Score 358; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 1.1e-28;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      88  GKAFVKESLKCICANGVTSTKVFALIRGCTFORMIAEYQEECYSKLVNCSIAKRNPEALTE 147
      |||
Db      1  GKAFVKESLKCICANGVTSTKVFALIRGCTFORMIAEYQEECYSKLVNCSIAKRNPEALTE 60
QY      148 VVQLENNHFSN 157
      |||
Db      61 VVQLENNHFSN 70
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Search completed: November 22, 2004, 18:11:16  
Job time : 86 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2004, 16:07:12 ; Search time 377 Seconds  
(without alignments)  
7209.609 Million cell updates/sec

Title: US-09-705-500A-1

Perfect score: 503  
Sequence: 1 ctataatgcttcttacaata.....taataagtgcttacttta 503

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 362788 seqs, 2701811610 residues

Total number of hits satisfying chosen parameters: 7255776

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*  
2: /cgn2\_6/ptodata/2/pubpna/US06\_PCT\_NEW\_PUB.seq:\*  
3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*  
5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*  
7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*  
8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*  
9: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
10: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
11: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
12: /cgn2\_6/ptodata/2/pubpna/US09\_PUBCOMB.seq:\*  
13: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
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18: /cgn2\_6/ptodata/2/pubpna/US10\_PUBCOMB.seq:\*  
19: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
20: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*  
21: /cgn2\_6/ptodata/2/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	503	100.0	3765	13	US-10-044-090-638
2	503	100.0	3897	14	US-10-198-846-13651
3	458	91.1	3757	15	US-10-641-643-1502
4	458	91.1	3901	15	US-10-177-293-440
5	458	91.1	3901	15	US-10-465-572-117
6	458	91.1	3901	15	US-10-159-563-292
7	458	91.1	3901	16	US-10-372-683-40
8	458	91.1	3901	16	US-10-240-425-1425
9	393.4	78.2	572	16	US-10-152-319A-1327
10	229.4	45.6	263	9	US-09-880-107-249
11	224.8	44.7	563	10	US-09-814-353-18293
12	209.6	41.7	390	10	US-09-814-353-5522

13	209.6	41.7	390	10	US-09-814-353-11909	Sequence 11909, A
14	176.8	35.1	556	15	US-10-102-524-873	Sequence 873, App
15	60	11.9	60	10	US-09-908-975-1768	Sequence 1768, A
16	60	11.9	60	10	US-09-908-975-1919	Sequence 1919, A
17	55.8	11.1	3673778	15	US-10-312-841-2	Sequence 2, Appl1
18	53.4	11.0	6917	15	US-10-311-455-2208	Sequence 2208, Ap
19	55	10.9	12237	15	US-10-311-455-2331	Sequence 2331, Ap
20	54.8	10.9	19087	15	US-10-311-455-766	Sequence 766, App
21	54.6	10.9	6154	15	US-10-221-613-59	Sequence 69, Appl
22	53.6	10.7	5689	14	US-10-239-676-90	Sequence 90, Appl
23	53.6	10.7	5689	15	US-10-240-453-100	Sequence 100, App
24	53.6	10.7	5689	16	US-10-221-744A-148	Sequence 148, App
25	53.4	10.6	8254	15	US-10-311-455-837	Sequence 837, App
26	53.4	10.6	17234	17	US-10-433-793-838	Sequence 48, Appl
27	52.6	10.5	10328	15	US-10-311-455-1517	Sequence 1517, Ap
28	51.2	10.2	10333	15	US-10-311-455-1532	Sequence 432, App
29	51.2	10.2	37515	17	US-10-433-793-28	Sequence 28, Appl
30	51.2	10.2	3673778	15	US-10-312-841-1	Sequence 1, Appl1
31	51	10.1	15479	16	US-10-257-166-45	Sequence 45, Appl
32	50.8	10.1	5829	15	US-10-311-455-1700	Sequence 1700, Ap
33	50.8	10.1	6074	15	US-10-311-455-1038	Sequence 1038, Ap
34	50.8	10.1	8592	15	US-10-311-455-1955	Sequence 1955, Ap
35	50.6	10.1	15518	15	US-10-311-455-2145	Sequence 2145, Ap
36	50.6	10.1	15518	15	US-10-240-485-177	Sequence 177, App
37	50.4	10.0	5107	15	US-10-311-455-1039	Sequence 1039, Ap
38	50.4	10.0	14924	15	US-10-311-455-198	Sequence 198, App
39	50.4	10.0	14924	15	US-10-240-452-12	Sequence 12, Appl
40	50.2	10.0	9741	15	US-10-311-455-1296	Sequence 1296, Ap
41	50.2	10.0	16688	15	US-10-311-455-293	Sequence 293, App
42	49.8	9.9	5291	15	US-10-311-455-1292	Sequence 192, App
43	49.8	9.9	5291	15	US-10-240-452-58	Sequence 58, Appl
44	49.6	9.9	6092	15	US-10-221-613-36	Sequence 36, Appl
45	49.6	9.9	6352	15	US-10-172-086-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1  
US-10-044-090-638  
; Sequence 638, Application US/10044090  
; Publication No. US20020137081A1  
; GENERAL INFORMATION:  
; APPLICANT: Oiga Bandman  
; TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION  
; FILE REFERENCE: PA-0028 US  
; CURRENT APPLICATION NUMBER: US/10/044,090  
; CURRENT FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 850  
; SOFTWARE: PERL Program  
; SEQ ID NO 638  
; LENGTH: 3765  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; OTHER INFORMATION: Inocyte ID No. US20020137081A1 331181.1  
; LOCATION: 2378, 3184, 3187, 3194  
; OTHER INFORMATION: a, t, c, g, or other  
US-10-044-090-638  
Query Match 100.0%; Score 503; DB 13; Length 3765;  
Best Local Similarity 100.0%; Pred. No. 1e-101;  
Matches 503; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CTATTATGCTATCTTCACATATATCTTACAGTACAGAAAGAGAGAGTTCACATG 60  
DB 3255 CTAATATGATATCTTACAAATATATCTTACAGTACAGAAAGAGAGAGTTCACATG 3314  
QY 61 TTGCTAGTATTTTGGCTTCTTCTTCCACACCTTCCTCCATTCCTCCCTTAACTTC 120  
DB 3315 TTGCTAGTATTTTGGCTTCTTCTTCCACACCTTCCTCCATTCCTCCCTTAACTTC 3374

QY	121	CAAAGCTTCGCTCTGTGTTTCTGTCAGAGTGAATTCGGGGGCTGACCTTAGACAGTTTGCA	180
Db	3375	CAAAGCTTCGCTCTGTGTTTCTGTCAGAGTGAATTCGGGGGCTGACCTTAGACAGTTTGCA	3434
QY	181	TGATTCCTCTCTGTGATTTGGTTCGACCTTAGACATTTTGTGCCATTAATTTTGCATT	240
Db	3435	TGATTCCTCTCTGTGATTTGGTTCGACCTTAGACATTTTGTGCCATTAATTTTGCATT	3494
QY	241	ATGATATTATTAATTTAAATGCAATTTAGCTTTTGGCTGAGTACGAAATTAACAGTAG	300
Db	3495	ATGATATTATTAATTTAAATGCAATTTAGCTTTTGGCTGAGTACGAAATTAACAGTAG	3554
QY	301	CATATCTGGTATGTCATTTATTTATTTGTTAAATTTTACAATTTTAAAGTCCATGTGCATAT	360
Db	3555	CATATCTGGTATGTCATTTATTTATTTGTTAAATTTTACAATTTTAAAGTCCATGTGCATAT	3614
QY	361	AAAGGTATGAAACATATCATGTGTAATGACACATGCAAGTATATTATTGTCTATTTT	420
Db	3615	AAAGGTATGAAACATATCATGTGTAATGACACATGCAAGTATATTATTGTCTATTTT	3674
QY	421	ATAATTAAGAATGCCATATGCAATTAATATGAAAGCTTTGGTGAATTCCTCTTAAGATPAAAA	480
Db	3675	ATAATTAAGAATGCCATATGCAATTAATATGAAAGCTTTGGTGAATTCCTCTTAAGATPAAAA	3734
QY	481	TAAATATAAAGTGTACGTTTTA	503
Db	3735	TAAATATAAAGTGTACGTTTTA	3757

## RESULT 2

US-10-198-846-13651  
; Sequence 13651, Application US/10198846  
; Publication No. US2003009974A1  
; Publication No. US2003009974A1

```

1  GENERAL INFORMATION:
2  APPLICANT: Lillie, James
3  APPLICANT: Xu, Yongyao
4  APPLICANT: Wang, Youzhen
5  APPLICANT: Steimann, Kathleen
6  TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
7  TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
8  TITLE OF INVENTION: THERAPY OF BREAST CANCER
9  FILE REFERENCE: WFI-049
10 CURRENT APPLICATION NUMBER: US/10/198,846
11 CURRENT FILING DATE: 2002-07-18
12 PRIOR APPLICATION NUMBER: 60/306,220
13 PRIOR FILING DATE: 2001-07-18
14 NUMBER OF SEQ ID NOS: 14084
15 SOFTWARE: PasteSeq for Windows Version 4.0
16 SEQ ID NO 13651
17
18 LENGTH: 3897
19
20 TYPE: DNA
21
22 ORGANISM: Homo sapiens
23
24 FEATURE:
25 NAME/KEY: misc_feature
26 LOCATION: 3878..3879, 3880..3881, 3882..3883, 3884..3885, 3886..3887
27 LOCATION: 3888..3889, 3890..3891, 3892..3893, 3894..3895, 3896..3897
28 OTHER INFORMATION: n = A,T,C or G
29
30 US-10-198-846-13651

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Query Match	100.0%	Score 503;	DB 14;	Length 3897
Best Local Similarity	100.0%	Pred. No. 1e-101;		
Matches 503;	Conservative	0;	Mismatches	0;

OY	1	CTAATATGATGATCAATACATATATCTACACATACGAAAGAGCGCTTCGCATG	60
Db	3367	CTAATATGATGATCAATACATATATCTACACATACGAAAGAGCGCTTCGCATG	3422
OY	61	TTGCTAGATTTTTGCTCTCTTTCCGCCACCGCTACCTGCGAATTCGCCCTTAAATCTC	120
Db	3427	TTGCTAGATTTTTGCTCTCTTTCCGCCACCGCTACCTGCGAATTCGCCCTTAAATCTC	3483
OY	121	CAAGCTTCGCTCTGTTGTTGCTGCAGAGTGATTCGGGGGCTGACCTTAGACCAATTTTGA	180

Dd	3487	CAAAGCTTCGGCTTCCTGCTGCTTGGCTGCAAGAGATTTCGGGGGGCTGCACCTAGACCAATTGGCA	3546
Qy	181	TGATTCCTCTCTTGGWATTTGGTTGCACCTTTAGACATTTTGGGCCATATATTTGGCAT	240
Dd	3547	TGATTCCTCTCTTGGATTTGGTTGGCACTTTAGACATTTTGGGCCATATATTTGGCAT	3606
Qy	241	ATGATTTTAAATTTAAATGATATTTAGTTTGGCTGGAGTACTGGAAATTAACAGTGAG	300
Dd	3607	ATGATTTTAAATTTAAATGATATTTAGTTTGGCTGGAGTACTGGAAATTAACAGTGAG	3666
Qy	301	CATATCTGATATATGTCATTATTTATTTGTTAAATTAATTCATTTTAACTGCATGTCAT	360
Dd	3667	CATATCTGATATATGTCATTATTTATTTGTTAAATTAATTCATTTTAACTGCATGTCAT	3726
Qy	361	AAAGGTTATGAAACATATCATGCTGAATGACAGATGCAGATTTTATTTGGCTATTTT	420
Dd	3727	AAAGGTTATGAAACATATCATGCTGAATGACAGATGCAGATTTTATTTGGCTATTTT	3786
Qy	421	ATATTTAAAGTTGGCATATGCAATATATGAAAGCTTTGGTGAATCCCTCTAAGATAAAA	480
Dd	3787	ATATTTAAAGTTGGCATATATGCAATATATGAAAGCTTTGGTGAATCCCTCTAAGATAAAA	3846
Qy	481	TAAATATTAAGTCTTAAGCTTTTA	503
Dd	3847	TAAATATTAAGTCTTAAGCTTTTA	3869

### RESULT 3

US-10-641-643-1502  
; Sequence 1502, Application US/10641643  
; Publication No. US20040077003A1  
GENERAL INFORMATION

GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G  
Susan G. Stuart  
Telford, T. Coilher

JEFFREY D. SELLINGER  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL  
GENE EXPRESSION

NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC

STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA

```
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM
```

```

;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: IBM PC compatible
;
; OPERATING SYSTEM: PC-DOS/MS-DOS
;

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; SOFTWARE: Word Perfect 6.1 for Windows
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/641,643

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FILING DATE: 14-Aug-2003  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166

```

;
; INFORMATION FOR SEQ ID NO: 1502:
;     SEQUENCE CHARACTERISTICS:
;         LENGTH: 3757 base pairs

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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

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IMMEDIATE SOURCE:  
LIBRARY: GENBANK

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; CLONE: g975297
; SEQUENCE DESCRIPTION: SEQ ID NO: 1502 :
US-10-641-643-1502

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Query Match	91.1%;	Score 458;	DB 16;	Length 3757;
Best Local Similarity	99.2%;	Pred. No. 1e-91;		
Matches 502; Conservative	0;	Mismatches 0;	Indels 4;	Gaps 4;

QY	1	CTAATATATGTAATCAATACATATATCTACACATACAGAAAGAACAGTCTCCAAATG	60
Db	3244	CTAATATATGTAATCAATACATATATCTACACATACAGAAAGAACAGTCTCCAAATG	3302
QY	61	TTGCTAGTTTTTGTCTCTCTTTCCCAACCCCTATCCCTCCAAAT - CCCCCTAACTT	119
Db	3303	TTGCTAGTTTTTGTCTCTCTTTCCCAACCCCTATCCCTCCAAATTTCCCCCTTAAACTT	3362
QY	120	CCAAGACTCGCTGTGTGTGGCTSCAGAGTCATTCGGGGGGCTGACCTAGACCAAGTTGC	179
Db	3363	CCAAGACTCGCTGTGTGTGGCTSCAGAGTCATTCGGGGGGCTGACCTAGACCAAGTTGC	3422
QY	180	ATGATTTCTTCTCTGTGTGATTTGGTTGCACCTTACACATTTTGTGCCATATATTTGCAT	239
Db	3423	ATGATTTCTTCTCTGTGTGATTTGGTTGCACCTTACACATTTTGTGCCATATATTTGCAT	3482
QY	240	TATGATTTATTAATTTAAATGATATTTAGTTGGTTTGGCTGAGTATGGAATPAAACAGTGA	299
Db	3483	TATGATTTATTAATTTAAATGATATTTAGTTGGTTTGGCTGAGTATGGAATPAAACAGTGA	3544
QY	300	GCAATATCTGTATATGTCAATTTATTTGTAAATTACA - TTTTAAAGCTCATGTGCAT	358
Db	3543	GCAATATCTGTATATGTCAATTTATTTGTAAATTACAATTTTAAAGCTCATGTGCAT	3602
QY	359	ATTAAGGTTATGAAGACATATCATGTGATATGACAGATGCAAGTATTTTATTTTGGCTTA - TT	417
Db	3603	ATTAAGGTTATGAAGACATATCATGTGATATGACAGATGCAAGTATTTTATTTTGGCTTAATTT	3662
QY	418	TTTATTAATTAAGAATGCATATGCAATTAATATGAAGCTTTGGTGAATTCCTCTAAGATTA	477
Db	3663	TTTATTAATTAAGAATGCATATGCAATTAATATGAAGCTTTGGTGAATTCCTCTAAGATTA	3722
QY	478	AAATTAATTAATAAGCTTACGTTTTTA 503	
Db	3723	AAATTAATTAATAAGCTTACGTTTTTA 3748	

RESULT 4  
US-10-177-293-440  
; Sequence 440, Application US/10177293

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? PRIOR APPLICATION NUMBER: US 60/229,887
? PRIOR FILING DATE: 2001-06-21
? PRIOR APPLICATION NUMBER: US 60/301,572
? PRIOR FILING DATE: 2001-06-27
? PRIOR APPLICATION NUMBER: US 60/306,501
? PRIOR FILING DATE: 2001-07-18
? PRIOR APPLICATION NUMBER: US 60/325,002
? PRIOR FILING DATE: 2001-09-25
? PRIOR APPLICATION NUMBER: US 60/365,585
? PRIOR FILING DATE: 2002-03-05
? PRIOR APPLICATION NUMBER: US 60/xxx,xxx
? PRIOR FILING DATE: 2002-05-14
? NUMBER OF SEQ ID NOS: 506
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 440
? LENGTH: 3901
? TYPE: DNA
? ORGANISM: Homo sapiens
US-10-177-293-440

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Query Match	91.1%;	Score 458;	DB 15;	Length 3901;
Best Local Similarity	99.2%;	Pred. No. 1.1e-91;		
Matches 502; Conservative	0;	Mismatches	0;	Indels 4; Gaps 4;

QY	1	CTATATATGATCTACAAATACATATATCTCACAATACAGAAAGAGAGTTCTCACATG	60
Db	3369	CTATATATGATCTACAAATACATATATCTCACAATACAGAAAGAGAGTTCTCAC-ATG	3427
QY	61	TTGGTAGTTTTTGGCTTCTCTTTCGCCACCTTAATCTCCCTCCAAAT-CCCCCTTAACTT	119
Db	3428	TTGGTAGTTTTTGGCTTCTCTTTCGCCACCTTAATCTCCCTCCAAATTCCTCCCTTAAACTT	3487
QY	120	CCAAAGCTTGCTGTGTTGTGCTGCAGAGNGATTTGGGGGCTGACCTAGACAGTTGTC	179
Db	3488	CCAAAGCTTGCTGTGTTGTGCTGCAGAGTGAATTCGGGGGCTGACCTAGACAGTTTGC	3547
QY	180	ATGATTTCTTCTCTTGATTTGGTTGGTCAGTTTAGACAATTTTGTGCATTAATATTTGCAT	239
Db	3548	ATGATTTCTTCTCTTGATTTGGTTGGTCAGCTTTAGACAATTTTGTGCATTAATATTTGCAT	3607
QY	240	TATGATTTTAATTTTAATGATATATTAAGTTTTGGCTAGTACATGGAATTAACAGTGA	299
Db	3608	TATGATTTTAATTTTAATGATATATTAAGTTTTGGCTAGTACATGGAATTAACAGTGA	3667
QY	300	GCAATATCTGCTATATGTCATTATTTATTTGTTAAATTACA-TTTTAAAGCTCCATGTCAT	358
Db	3668	GCAATATCTGCTATATGTCATTATTTATTTGTTAAATTACAATTTTAAAGCTCCATGTCAT	3727
QY	359	ATAAAGTTATGAAACAATATCATAGGTATATACAGATGCAAGTATTTTATTTTGGTTA-TT	417
Db	3728	ATAAAGTTATGAAACAATATCATAGGTATATACAGATGCAAGTATTTTATTTTGGTTATTT	3787
QY	418	TTTATATTTAAAGATGCGCATAGACATATATGAAGCCTTTGATGATTCCTTCTTAAGATAA	477
Db	3788	TTTATATTTAAAGATGCGCATAGACATATATGAAGCCTTTGATGATTCCTTCTTAAGATAA	3847
QY	478	AAATATATTAATAAAGCTTACGTTTTA	503
Db	3848	AAATATATTAATAAAGCTTACGTTTTA	3873

RESULT 5  
US-10-465-572-17  
; Sequence 17, Application US/10465572  
; Publication No. US20030207840A1

```

? RESULT 6
? US-10-159-563--292
? Sequence 292, Application US/10159563
? Publication No. US20040009154A1
? GENERAL INFORMATION:
? APPLICANT: Khan, Javed
? APPLICANT: Ringner, Markus
? APPLICANT: Peterson, Carsten
? APPLICANT: Meltzer, Paul
? TITLE OF INVENTION: SELECTIONS AND METHODS OF USING THE SAME FOR
? TITLE OF INVENTION: DIAGNOSIS AND FOR TARGETING THE THERAPY OF SELECT CANCERS
? FILE REFERENCE: 11613.360S11
? CURRENT APPLICATION NUMBER: US/10/159,563
? CURRENT FILING DATE: 2002-12-09
? PRIOR APPLICATION NUMBER: US 10/133,937
? PRIOR FILING DATE: 2002-04-25
? NUMBER OF SEQ ID NOS: 444
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 292
? LENGTH: 3901
? TYPE: DNA
?

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Query Match	91.1%	Score 458;	DB 16	Length 3901;
Best Local Similarity	99.2%	Pred. NO. 1.1e-91;		
Matches	502;	Conservative	0;	Mismatches 4; Gaps 4

1 CTATTATGATCTACATATATCTATACACATACGAAAGACGTTCTCAATG 60  
 |||

Db	3369	CTATATATAGTATCTTACAAATACATATATATCTACATACATGAAAGAAAGAGCTTCTCAC-ATG	3427
Qy	61	TTGCTAGTTTTTTTGGTTCTCTCTTTGCCCAACCTTACTCCTTCCAAAT-CCCCCTTAACTT	119
Db	3428	TTGCTAGTTTTTTTGGTTCTCTCTTTCCCCACCCCTACTCCTTCCAAATCCCCCTTAACTT	3487
Qy	120	CCAAAGCTCGCTGTTGTGTGTGCTGCAGAGTGCATGCGGAGGCTGACCTPAGACCAAGTTGCG	179
Db	3488	CCAAAGCTCGCTGTTGTGTGTGCTGCAGAGTGCATGCGGAGGCTGACCTPAGACCAAGTTGCG	3547
Qy	180	ATGATCTCTCTCTTGATGATTTGGTTGCACCTTAAACATTTTTGTGCATTAATTTGCAT	239
Db	3548	ATGATCTCTCTCTTGATGATTTGGTTGCACCTTAAACATTTTTGTGCATTAATTTGCAT	3607
Qy	240	TATGATTTTAAATTTTAAATATATTTAGTTTTTGGCTGAGTACGTGAATPAAACAGTGA	299
Db	3608	TATGATTTTAAATTTTAAATATATTTAGTTTTTGGCTGAGTACGTGAATPAAACAGTGA	3667
Qy	300	GCATATCTGTATATATGTCATTATTTATTTGTTAAATTACA-TTTTAACTCCATGTCAT	358
Db	3668	GCATATCTGTATATATGTCATTATTTATTTGTTAAATTACATTTTAACTCCATGTCAT	3727
Qy	359	ATAAAGTTATGAACAATCATGCTATATGACATGCAATGCAATTTTATTTTGGCTTA-TT	417
Db	3728	ATAAAGTTATGAACAATCATGCTATATGACATGCAATGCAATTTTATTTTGGCTATTT	3787
Qy	418	TTTATTAATTAAGAATGCATATGCAATTAATTAAGAAGCTTTGGTGAATTCCTCTAAGATTA	477
Db	3788	TTTATTAATTAAGAATGCATATGCAATTAATTAAGAAGCTTTGGTGAATTCCTCTAAGATTA	3847
Qy	478	AAATATATATTAAGTTTACGTTTTA	503
Db	3848	AAATATATATTAAGTTTACGTTTTA	3873

QY	6	TTGGTACATTTTTCCTCTGCTTCCTCCCCACCCATCTCCCTCAATT--CCCCCTTAAACTT	115
Db	3428	TTGGTACATTTTTCCTCTCTCTTCCCCACCCCTACTCCCTCCAATTCGCCCTTAACTT	3487
QY	120	CCAAAGCTTCGTCTGTGTTCCTGCAGAGTGAATCGG9363CTGACCTTAGCCAGTTTC	179
Db	3488	CCAAAGCTTCGTCTGTGTTCCTGCAGAGTGAATCGG9363CTGACCTTAGCCAGTTTC	3547
QY	180	ATGATTCCTCTCTGATTTGGTGGACCTTTAGACATTTTTCGGCATATATTGCAT	239
Db	3548	ATGATTCCTCTCTGATTTGGTGGACCTTTAGACATTTTTCGGCATATATTGCAT	3607
QY	240	TATGATTTTAAATTAAATGAATATTAGGTTTTTGCTGAGTACTGGAATAAACAGTGA	299
Db	3608	TATGATTTTAAATTAAATGAATATTAGGTTTTTGCTGAGTACTGGAATAAACAGTGA	3667
QY	300	GCAATCTCGTAAATGTCATTTATTATTGTTAAATTACA--TTTTAGCTCCAGTGCAT	358
Db	3668	GCAATCTCGTAAATGTCATTTATTATTGTTAAATTACAATTTTTAAAGCTCCAGTGCAT	3727
QY	359	ATAAAGTTAATGAACAATCATCATGTAATGCAGATSCAAGTTATTTTATTTCCTA--TT	417
Db	3728	ATAAAGTTAATGAACAATCATCATGTAATGCAGATSCAAGTTATTTTATTTCCTAATT	3787
QY	418	TTTATTAATTAAAGATGCGATTCGCAATTAATGAAAGCCTTTGGTGAATTCCTCTAAGATTA	477
Db	3788	TTTATTAATTAAAGATGCGATTCGCAATTAATGAAAGCCTTTGGTGAATTCCTCTAAGATTA	3847
QY	478	AAATTAATTAATTAAGTGTACGTTTTA	503
Db	3848	AAATTAATTAATTAAGTGTACGTTTTA	3873

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RESULT 8
US-10-240-425-1425
? Sequence 1425, Application US/10240425
? Publication No. US20040033502A1
? GENERAL INFORMATION:
? APPLICANT: Williams, Amanda
? APPLICANT: Boland, Joseph F.
? APPLICANT: Lord, Reginald V.
? APPLICANT: Alvarez, Chris
? APPLICANT: Wetzel, Jon C.
? APPLICANT: Scherf, Uwe
? APPLICANT: Vockley, Joseph G.
? TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue
? FILE REFERENCE: 44921-5026
? CURRENT APPLICATION NUMBER: US/10/240,425
? PRIOR FILING DATE: 2002-09-30
? PRIOR APPLICATION NUMBER: PCT/US01/09847
? PRIOR FILING DATE: 2001-03-28
? PRIOR APPLICATION NUMBER: US 60/193,446
? PRIOR FILING DATE: 2000-03-31
? NUMBER OF SEQ ID NOS: 1588
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 1425
? LENGTH: 3901
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURES:
? OTHER INFORMATION: Genbank Accession No. US20040033502A1 U25997
US-10-240-425-1425

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RESULT 9  
US-10-152-319A-1327/C  
Sequence 1327, Application US/10152319A  
Publication No. US20040072160A1  
GENERAL INFORMATION:  
APPLICANT: Mendrick, Donna  
APPLICANT: Porter, Mark  
APPLICANT: Johnson, Kory  
APPLICANT: Higgs, Brandon  
APPLICANT: Castle, Arthur  
APPLICANT: Elashoff, Michael  
TITLE OF INVENTION: Molecular Toxicology Modeling  
FILE REFERENCE: 44921-5089-US  
CURRENT APPLICATION NUMBER: US/10/152.319A  
CURRENT FILING DATE: 2002-05-22  
PRIOR APPLICATION NUMBER: US 60/292,335  
PRIOR FILING DATE: 2001-05-22  
PRIOR APPLICATION NUMBER: US 60/297,523  
PRIOR FILING DATE: 2001-06-13  
PRIOR APPLICATION NUMBER: US 60/298,925  
PRIOR FILING DATE: 2001-06-19  
PRIOR APPLICATION NUMBER: US 60/303,810  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/303,807  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/303,808  
PRIOR FILING DATE: 2001-07-10  
PRIOR APPLICATION NUMBER: US 60/315,047  
PRIOR FILING DATE: 2001-08-28  
PRIOR APPLICATION NUMBER: US 60/324,928  
PRIOR FILING DATE: 2001-09-27

Query Match	Similarity	Score	DB	Length
Best Local	99.2%	Pred. No. 1	1e-91	
Matches	502	Conservative	0	Indels 4; Gaps 4
Qy	1	CTAATATGATCTTCAATATACATATATCTTACACATACAGAAAGAGCAGTTCTCCAAATG	60	
Sb	3369	CTAATATGATCTTCAATATACATATATCTTACACATACAGAAAGAGCAGTTCTCCAC-ATG	3422	

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; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: US 60/330,462
; PRIOR FILING DATE: 2001-10-22
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 2221
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1327

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; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. AI235210
US-10-152-319A-1327

Query Match          78.2%; Score 393.4; DB 16; Length 572;
Best Local Similarity 91.5%; Pred. No. 1.2e-77;
Matches 453; Conservative 0; Mismatches 31; Indels 11; Gaps 3;

QY 4 TATATGATCTACATCATATATCTTACACATACAGAAAGAAAGAACTTCTCCAAAGTGG 63
DB 510 TATATGATCAACAATACATATATCTACACATATGAAAGAAAGAACTTCTCCAAAGTGG 451
QY 64 CTAGTTTCTGCTTCTCTT-----CCCCACCCCTACTCCCTCCCAATTCCTCCCTTAA 115
DB 450 CTAGTTTCTGCTTCTCTTCTTCTTCTCCACCCCTCCGCTCCCTCTCCACCTCTCTTAA 391
QY 116 ACTTCCAAAGCTTGCTTCTGTTTGTGCTGCAAGTGATTCGGGGGCTGACCTTAGACCACT 175
DB 390 ACTTCCAAAGCTTCTTCTGTTTGTGCTGCAAGTGATTCGGGGGCTGACCTTAGACCACT 331
QY 176 TTGATATATCTCTCTGTTGATTTGGTTCACCTTTAG-ACATTTTGTGCAATATAT 234
DB 330 TTGCAATAT--CTCTCCGGAATTTGGTTGCACTTTAGAACATTTTGTGCGCTTATAT 273
QY 235 TGCATATGATTTTAAATTTAAATGATTTAGTTTGGCTGAGTACTGGAAATTAAC 294
DB 272 TGCATATGATTTTAAATTTAAATGATTTAGTTTGGCTGAGTACTGGAAATTAAC 213
QY 295 AGTGAAGATATCTGATATATGTCATTTATTTATTTAAATTAATTTAAAGCTCCACT 354
DB 212 AGTGAAGATATCTGATATATGTCATTTATTTATTTAAATTTAAAGCTCCACT 153
QY 355 GCATATTAAGGTTATGAAACATATCATGTATGACAGATGACAGTATTTATTTGCTT 414
DB 152 GCATATTAAGGTTATGAAACATATCATGTATGACAGATGACAGTATTTATTTGCTT 93
QY 415 ATTTTATATTAAGTGCATATGATATATGAAAGCTTGGTGAATTCCTCTTAAGA 474
DB 92 ATTTTATATTAAGTGCATATGATATTTGAAGCTTGGTGAATTCCTCTTAAGA 33
QY 475 TAAAAATATATATTA 489
DB 32 TAAATATATATATTA 18

RESULT 10
US-09-880-107-249/c
; Sequence 249, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Schert, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-NO
; CURRENT APPLICATION NUMBER: US/09/880,107
; PRIOR FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 249
; LENGTH: 263
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA126561
NAME/KEY: unsure
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; LOCATION: (1)..(263)
; OTHER INFORMATION: n = a or c or g or t
US-09-880-107-249

Query Match          45.6%; Score 229.4; DB 9; Length 263;
Best Local Similarity 95.7%; Pred. No. 2.6e-41;
Matches 244; Conservative 0; Mismatches 10; Indels 1; Gaps 1;

QY 249 ATAATTTAAATGATTTAGTTTGGCTGAGTACTGATTAACAGTAGCATATCTG 308
DB 263 ATAATTTAAATGATTTAGTTTGGCGGAGTACTGANT-AACAGNAGCATATCTG 205
QY 309 GTATATGTCATTTATTTGTTAAATTAATTAATTAAGCTCCATGTCATTAAGTTA 368
DB 204 GTATATGTCATTTATTTGTTAAATTAATTAATTAAGCTCCATGTCATTAAGTTA 145
QY 369 TGAACATATCATGTATGACAGATGCAAGTTATTTATTTGCTATTTTAAATTA 428
DB 144 TGAACATATCATGTATGACAGATGCAAGTTATTTATTTGCTATTTTAAATTA 85
QY 429 AGATGCAATGACATATATATGAGCTTTGGTGAATTCCTCTTAAGATTAATAATA 488
DB 84 AGATGCAATGACATATATATGAGCTTTGGTGAATTCCTCTTAAGATTAATAATA 25
QY 489 AAGTTTACGTTTAA 503
DB 24 AAGTTTACGTTTAA 10

RESULT 11
US-09-814-353-18293
; Sequence 18293, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lillie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: KRI-0068
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18293
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 466, 467, 468, 470, 471, 473, 475, 490, 520, 521
; OTHER INFORMATION: n = A,T,C or G
US-09-814-353-18293

Query Match          44.7%; Score 224.8; DB 10; Length 563;
Best Local Similarity 99.1%; Pred. No. 3.6e-40;
Matches 226; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 276 GCTGAGTACTGGAATTAACAGTGAATATCTGTATATCTCATTTATTTGTTAAAT 335
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Db      228 GGTAGTACTGGAATAAACAAGTACGATATCTGGTATATGTCATTTATTTTGTAAATT 287
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lilie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5622
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5622
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## RESULT 12

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US-09-814-353-5622
; Sequence 5622, Application US/09814353
; Publication No. US20030165831A1
; GENERAL INFORMATION:
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; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lilie, James
```

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; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5622
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-5622
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Query Match      41.7%; Score 209.6; DB 10; Length 390;
Best Local Similarity 97.8%; Pred. No. 7.6e-37;
Matches 223; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
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Db      276 GCTGAGTACTGGAATAAACAAGTACGATATCTGGTATATGTCATTTATTTTGTAAATT 335
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Mannion, Jane A.
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-102-524-873
```

```
US-10-102-524-873
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mannion, Jane A.
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-102-524-873
```

```
; Publication No. US20030165831A1
; GENERAL INFORMATION:
; APPLICANT: Lee, John
; APPLICANT: Thompson, Pamela
; APPLICANT: Lilie, James
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS FOR
; TITLE OF INVENTION: IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-006B
; CURRENT APPLICATION NUMBER: US/09/814,353
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: US 60/191,031
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: US 60/207,124
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 60/211,940
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: US 60/216,820
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/220,661
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/257,672
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 22037
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11909
; LENGTH: 390
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-814-353-11909
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Query Match      41.7%; Score 209.6; DB 10; Length 390;
Best Local Similarity 97.8%; Pred. No. 7.6e-37;
Matches 223; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
```

```
Db      276 GCTGAGTACTGGAATAAACAAGTACGATATCTGGTATATGTCATTTATTTTGTAAATT 335
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Mannion, Jane A.
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-102-524-873
```

```
US-10-102-524-873
; Sequence 873, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mannion, Jane A.
; APPLICANT: Gauger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102,524
; PRIOR FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 873
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-102-524-873
```

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RESULT 13
US-09-814-353-11909
; Sequence 11909, Application US/09814353
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FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 327, 343, 510, 543  
OTHER INFORMATION: n = A,T,C or G  
US-102-524-873

Query Match 35.1%; Score 176.8; DB 15; Length 556;  
Best Local Similarity 97.8%; Pred. No. 1.7e-29;  
Matches 178; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CTATATATGATCTACATATATATCTACATACAGAAAGACAGTTCTCACATG 60  
DB 375 CTATATATGATCTACAGTACATATATCTACATACAGAAAGACAGTTCTCACATG 434  
QY 61 TTGCTAGTTTTCCTCTCTTCCGCCACCTACTCCCTCAATCCCTTAACTTC 120  
DB 435 TTGCTAGTTTTCCTCTCTTCCGCCACCTACTCCCTCAATCCCTTAACTTC 494  
QY 121 CAAAGCTCGCTGTTGTTGCTGACAGATTCGGGGCTGACCTAGACAGTTTGA 180  
DB 495 CAAAGCTCGCTGTTGTTGCTGACAGATTCGGGGCTGACCTAGACAGTTTGA 554  
QY 181 TG 182  
DB 555 TG 556

## RESULT 15

US-09-908-975-31768  
Sequence 31768, Application US/09908975  
Publication No. US20030165843A1  
GENERAL INFORMATION:  
APPLICANT: SHOSHAN, Avi  
APPLICANT: MASSEMAN, Alon  
APPLICANT: MINTZ, Eli  
APPLICANT: FALGER, Simchon  
TITLE OF INVENTION: OLIGONUCLEOTIDE LIBRARY FOR DETECTING RNA TRANSCRIPTS AND SPLIC  
FILE REFERENCE: 36688-0005  
CURRENT APPLICATION NUMBER: US/09/908,975  
CURRENT FILING DATE: 2001-07-20  
PRIOR APPLICATION NUMBER: US 60/287,724  
PRIOR FILING DATE: 2001-05-02  
PRIOR APPLICATION NUMBER: US 60/221,607  
PRIOR FILING DATE: 2000-07-28  
NUMBER OF SEQ ID NOS: 32337  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 31768  
LENGTH: 60  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-908-975-31768

Query Match 11.9%; Score 60; DB 10; Length 60;  
Best Local Similarity 100.0%; Pred. No. 0.00069;  
Matches 60; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 GTGATTGGGGGCTGACCTAGACAGTTGATTTCTTGTGATTTGGTTGAC 208  
DB 1 GTGATTGGGGGCTGACCTAGACAGTTGATTTCTTGTGATTTGGTTGAC 60

Search completed: November 22, 2004, 17:49:21  
Job time : 386 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 22, 2004, 16:51:37 ; Search time 19.5 Seconds  
(without alignments)  
3421.329 Million cells updates/sec

Title: US-09-705-500A-1  
Sequence: 1 ccatatcatctacatacaata.....taataaagtctacgttcta 503

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=rlh  
-Q=/cgn2\_1/usfto\_spool/us09705500/runat.22112004.073621.19217/app.query.fasta\_1.647  
-DB=Issued Patents\_AA -QPM=fastan -SUFFIX=ra1 -MINMATCH=0.1 -LOOPCL=0  
-LOOPEXT=0 -UNITS=BITS -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi  
-LIST=45 -DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTMT=plc -NOB=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US09705500 @CEN 1.1.22 @runat.22112004.073621.19217 -NCPU=6 -ICPU=3  
-NO\_MMAP -IAR=SEQUERY -NEG\_SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOC  
-DEV\_TIMEOUT=120 -MAIN\_TIMEOUT=30 -THEREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PCTUS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfilest1.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	75	8.6	144	2	US-08-950-168-1 Sequence 1, Appl
2	75	8.6	144	3	US-09-365-705-1 Sequence 1, Appl
3	75	8.6	144	4	US-09-702-705-327 Sequence 327, App
4	75	8.6	144	4	US-09-736-457-327 Sequence 327, App
5	75	8.6	144	4	US-09-614-124B-327 Sequence 327, App
6	75	8.6	144	4	US-09-671-325-327 Sequence 327, App
7	75	8.6	144	4	US-09-589-184-327 Sequence 327, App
8	75	8.6	144	4	US-09-658-824-327 Sequence 327, App
9	75	8.6	145	4	US-09-257-179-63 Sequence 63, Appl
10	74.5	8.5	664	4	US-09-823-038A-48 Sequence 48, Appl
11	72.5	8.2	330	4	US-09-270-767-46166 Sequence 46166, A
12	71.5	8.2	353	4	US-09-270-767-34960 Sequence 34960, A

13	71.5	8.2	353	4	US-09-270-767-50177 Sequence 50177, A
14	70.5	8.1	63	4	US-09-248-796A-27951 Sequence 27951, A
15	70.5	8.1	405	4	US-09-134-000C-5472 Sequence 5472, Ap
16	70	8.0	315	4	US-09-248-796A-15178 Sequence 15178, A
17	68	7.8	248	4	US-09-270-767-38407 Sequence 38407, A
18	68	7.8	248	4	US-09-270-767-53624 Sequence 53624, A
19	68	7.8	440	4	US-09-270-767-46800 Sequence 46800, A
20	68	7.7	960	3	US-09-345-650-1 Sequence 1, Appl
21	67.5	7.7	266	4	US-09-270-767-34032 Sequence 34032, A
22	67.5	7.7	266	4	US-09-270-767-49249 Sequence 49249, A
23	67	7.7	103	4	US-09-270-767-18215 Sequence 38215, A
24	67	7.7	103	4	US-09-270-767-53432 Sequence 53432, A
25	67	7.6	254	4	US-09-568-106D-93 Sequence 93, Appl
26	66.5	7.6	372	4	US-09-668-097A-14 Sequence 14, Appl
27	66	7.6	354	4	US-09-270-767-39281 Sequence 39281, A
28	66	7.6	354	4	US-09-270-767-54498 Sequence 54498, A
29	65.5	7.5	515	3	US-08-796-899-24 Sequence 24, Appl
30	65.5	7.4	587	4	US-09-270-767-37567 Sequence 37567, A
31	65.5	7.4	587	4	US-09-270-767-52784 Sequence 52784, A
32	65	7.4	133	3	US-09-384-162-16395 Sequence 16, Appl
33	65	7.4	149	4	US-09-270-767-43975 Sequence 43975, A
34	65	7.4	237	4	US-09-270-767-40963 Sequence 40963, A
35	65	7.4	237	4	US-09-270-767-56179 Sequence 56179, A
36	65	7.4	716	4	US-09-270-767-42322 Sequence 42322, A
37	64.5	7.3	603	2	US-08-687-865A-2 Sequence 2, Appl
38	64.5	7.3	603	3	US-09-043-711-3 Sequence 210, App
39	64.5	7.4	677	4	US-10-140-002-230 Sequence 6555, Ap
40	64	7.2	206	4	US-09-543-681A-6555 Sequence 15999, A
41	64	7.2	239	4	US-09-248-796A-15999 Sequence 41529, A
42	64	7.2	513	4	US-09-270-767-11529 Sequence 36669, A
43	63.5	7.2	153	4	US-09-270-767-11866 Sequence 51866, A
44	63.5	7.2	153	4	US-09-270-767-51866 Sequence 20444, A
45	63.5	7.3	228	4	US-09-248-796A-20444 Sequence 20444, A

#### ALIGNMENTS

RESULT 1  
US-08-950-168-1  
; Sequence 1, Application US/08950168  
; Patent No. 5968744  
; GENERAL INFORMATION:  
; APPLICANT: Hillman, Jennifer L.  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: HUMAN CORNICHON PROTEIN  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/950,168  
; FILING DATE: Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J.  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0401 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-855-0555  
; TELEFAX: 650-845-4166

TELEX:  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 144 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADNOT04  
CLONE: 1318847  
US-08-950-168-1

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-08-950-168-1 (1-144)

QY 142 CTGCAAGTATTCGGGGGCTGACCTAGACCACTTGCATGATTCCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuYsthrAspYrYrYsaenProIleaspGln-----CysaenThr 47  
|||:|||||  
QY 202 -----CTGCACCTTGAACATTTTGTGCCAT---TATATTGCATTAGATTTA 249  
|||:|||||  
Db 48 LeuasnProLeuValLeuProGluYrLeuIleHisAlaPheheCysValMetPheLeu 67  
|||:|||||  
QY 250 TAATTTAAATGATATTAGGTTTGTGCTGAGTACTGGAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaIaIaGluTPrLeuThrLeuGlyLeuasnMetProLeuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTCA----- 318  
|||:|||||  
Db 84 TyrHisIleTPrArgYrMetSerArgProValMetSerGlyProGlyLeuYrAspPro 103  
|||:|||||  
QY 319 TTATTATGTTAAATTTACATTTTAAAGCTCCATGTCATATAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetasnAlaaspIleLeuAlaIaTy-CysGlnMySgluGlyTrp----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420  
|||:|||||  
Db 121 -----CysLysLeuAlaPheTyLeuLeuAlaPhe 130  
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RESULT 2  
US-09-365-705-1  
Sequence 1, Application US/09365705  
Patent No. 6348576  
GENERAL INFORMATION:  
APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Shah, Purvi  
TITLE OF INVENTION: HUMAN CORNICHON PROTEIN  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
City: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/365,705  
FILING DATE: 02-Aug-1999  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/950,168

FILING DATE: 14-OCT-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0401 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 144 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: BLADNOT04  
CLONE: 1318847  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-365-705-1

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500a-1 (1-503) x US-09-365-705-1 (1-144)

QY 142 CTGCAAGTATTCGGGGGCTGACCTAGACCACTTGCATGATTCCTCTTGATTTG 201  
|||:|||||  
Db 34 LeuYsthrAspYrYrYsaenProIleaspGln-----CysaenThr 47  
|||:|||||  
QY 202 -----CTGCACCTTGAACATTTTGTGCCAT---TATATTGCATTAGATTTA 249  
|||:|||||  
Db 48 LeuasnProLeuValLeuProGluYrLeuIleHisAlaPheheCysValMetPheLeu 67  
|||:|||||  
QY 250 TAATTTAAATGATATTAGGTTTGTGCTGAGTACTGGAATAAAC-----AGT 297  
|||:|||||  
Db 68 -----CysAlaIaIaGluTPrLeuThrLeuGlyLeuasnMetProLeuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTCA----- 318  
|||:|||||  
Db 84 TyrHisIleTPrArgYrMetSerArgProValMetSerGlyProGlyLeuYrAspPro 103  
|||:|||||  
QY 319 TTATTATGTTAAATTTACATTTTAAAGCTCCATGTCATATAAGTTATGAACATAT 378  
|||:|||||  
Db 104 ThrThrIleMetasnAlaaspIleLeuAlaIaTy-CysGlnMySgluGlyTrp----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420  
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Db 121 -----CysLysLeuAlaPheTyLeuLeuAlaPhe 130  
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RESULT 3  
US-09-702-705-327  
Sequence 327, Application US/09702705  
Patent No. 6504010  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedrick, Tom  
APPLICANT: Carter, Derrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C14  
CURRENT APPLICATION NUMBER: US/09/702,705

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; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-702-705-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-702-705-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACAGATTGATGATCTCTCTTGATTTG 201
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 250 TAAATTAAATGATATTAGTTTGGCTGAGTACGTAGATAAAC-----AGT 297
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTGCATATAAGTTATGAACATAT 378
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyrP----- 120
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 379 CATGTATATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

RESULT 4
US-09-736-457-327
; Sequence 327, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-736-457-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACAGATTGATGATCTCTCTTGATTTG 201
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 250 TAAATTAAATGATATTAGTTTGGCTGAGTACGTAGATAAAC-----AGT 297
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTGCATATAAGTTATGAACATAT 378
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyrP----- 120
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 379 CATGTATATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

RESULT 5
US-09-614-124B-327
; Sequence 327, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-614-124B-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACAGATTGATGATCTCTCTTGATTTG 201
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 250 TAAATTAAATGATATTAGTTTGGCTGAGTACGTAGATAAAC-----AGT 297
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTGCATATAAGTTATGAACATAT 378
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyrP----- 120
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 379 CATGTATATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

```

```

Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-736-457-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACAGATTGATGATCTCTCTTGATTTG 201
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 250 TAAATTAAATGATATTAGTTTGGCTGAGTACGTAGATAAAC-----AGT 297
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTGCATATAAGTTATGAACATAT 378
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyrP----- 120
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 379 CATGTATATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

RESULT 5
US-09-614-124B-327
; Sequence 327, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedrick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-614-124B-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-614-124B-327 (1-144)
QY 142 CTGACAGATGATTGGGGGCTGACCTAGACAGATTGATGATCTCTCTTGATTTG 201
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 34 LeuYsthrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 202 -----GTGCACTTTAGACATTTTGTGCAT--TATATTGCATTATGATTTA 249
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 48 LeuAsnProIleValLeuProGluTyrLeuIleHisAlaPheCysValMetPheLeu 67
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 250 TAAATTAAATGATATTAGTTTGGCTGAGTACGTAGATAAAC-----AGT 297
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 68 -----CysAlaAlaGluTyrPleuThrLeuGlyLeuAsnMetProIleuAla 83
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 298 GAGCATATCTGG--TATATGTCA----- 318
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 84 TyrHisIleTyrPArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 319 TTATTATTGTTAAATTACATTTTAAAGCTCCATGTGCATATAAGTTATGAACATAT 378
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTyrP----- 120
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 379 CATGTATATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||
QY 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
Db |||:||||| |||:||||| |||:||||| |||:||||| |||:||||| |||:|||||

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```
Db 48 LeuasnProleuValLeuProGluTyrLeuIleHisAlaPheheCysValMetPheLeu 67
QY 250 TAATTAAATGATTAATTAGCTTTGGCTGAGTACTGCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuasnMetProleuLeuAla 83
QY 298 GAGCATATCTG---TATATGTC----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTAAATTAATTAATTTTAAAGTCCATGTCATTAATTAAGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATCAAGTTA---TTTATTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 6
US-09-671-325-327
; Sequence 327, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-671-325-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-671-325-327 (1-144)
QY 142 CTCGAGAGTGAATTCGGGGCTGACCTAGACAGTTCGATGATTCCTCTTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGACCTTTAGACATTTTGTGCCAT---TATATTGCATTAATGAATTA 249
Db 48 LeuasnProleuValLeuProGluTyrLeuIleHisAlaPheheCysValMetPheLeu 67
QY 250 TAATTAAATGATTAATTAGCTTTGGCTGAGTACTGCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuasnMetProleuLeuAla 83
QY 298 GAGCATATCTG---TATATGTC----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTAAATTAATTAATTTTAAAGTCCATGTCATTAATTAAGTTATGAACATAT 378
```

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Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATCAAGTTA---TTTATTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 7
US-09-589-184-327
; Sequence 327, Application US/09589184
; Patent No. 6664447
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaltanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Manion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; FILE REFERENCE: 210121.478C8
; CURRENT APPLICATION NUMBER: US/09/589,184
; CURRENT FILING DATE: 2000-06-05
; NUMBER OF SEQ ID NOS: 827
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 327
; LENGTH: 144
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-589-184-327

Alignment Scores:
Pred. No.: 0.153 Length: 144
Score: 75.00 Matches: 33
Percent Similarity: 41.74% Conservative: 15
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 4 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-589-184-327 (1-144)
QY 142 CTCGAGAGTGAATTCGGGGCTGACCTAGACAGTTCGATGATTCCTCTTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTGACCTTTAGACATTTTGTGCCAT---TATATTGCATTAATGAATTA 249
Db 48 LeuasnProleuValLeuProGluTyrLeuIleHisAlaPheheCysValMetPheLeu 67
QY 250 TAATTAAATGATTAATTAGCTTTGGCTGAGTACTGCAATAAC-----AGT 297
Db 68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuasnMetProleuLeuAla 83
QY 298 GAGCATATCTG---TATATGTC----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTAAATTAATTAATTTTAAAGTCCATGTCATTAATTAAGTTATGAACATAT 378
Db 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGlnLysTrp----- 120
QY 379 CATGGTAATGACAGATCAAGTTA---TTTATTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130

RESULT 8
US-09-658-824-327
; Sequence 327, Application US/09658824
; Patent No. 6746846
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
```

APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Pan, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
FILE REFERENCE: 210121.478C11  
CURRENT APPLICATION NUMBER: US/09/658,824  
CURRENT FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 1788  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 327  
LENGTH: 144  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-658-824-327

Alignment Scores:  
Pred. No.: 0.153 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9  
DB:

US-09-705-500a-1 (1-503) x US-09-658-824-327 (1-144)

QY 142 CTGCAAGATGATTCGGGGCTGACCTAGACCACTTGATTCCTCTTGATTTG 201  
|||:|||||  
DB 34 LeuylsthraspYrlysaenProileaspGln-----Cysaenthr 47  
|||:|||||  
QY 202 -----GTGCACCTTGACATTTTGTGCCAT---TATATTGCATTATGATTTA 249  
|||:|||||  
DB 48 LeuasnProleuValleuProgluYrleuIlehisAlaPheheCysValMetPheleu 67  
|||:|||||  
QY 250 TAAATTAATGATATTAGTTTGGCTGAGTACTGGAATAAAC-----AGT 297  
|||:|||||  
DB 68 -----CysAlaIaIaGlutPleuthrleuGlyLeuasnMetProleuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTC----- 318  
|||:|||||  
DB 84 TyhisIleTyrPargYrMetSerArgProValMetSerGlyProgluYrleuYrAspPro 103  
|||:|||||  
QY 319 TTATTATTGTAAATTACATTTTAACTCCATGTCATATATAAGTTATGAACATAT 378  
|||:|||||  
DB 104 ThrThrIleMetasnAlaAspIleleuAlaItyrCysGlnIySglInduIyTrrp----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGGCTTATTTT 420  
|||:|||||  
DB 121 -----CysIySleuAlaPheYrleuLeuAlaPhe 130  
|||:|||||

#### RESULT 9

US-09-257-179-63  
Sequence 63, Application US/09257179  
Patent No. 6410709  
GENERAL INFORMATION:  
APPLICANT: Ruben et al.  
TITLE OF INVENTION: 29 Human Secreted Proteins  
FILE REFERENCE: P2015P1  
CURRENT APPLICATION NUMBER: US/09/257,179  
CURRENT FILING DATE: 1998-02-25  
EARLIER APPLICATION NUMBER: PCT/US98/17709  
EARLIER FILING DATE: 1998-08-27  
EARLIER APPLICATION NUMBER: 60/056,270  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 60/056,271  
EARLIER FILING DATE: 1997-08-29  
EARLIER APPLICATION NUMBER: 60/056,247  
EARLIER FILING DATE: 1997-08-29

EARLIER APPLICATION NUMBER: 60/056,073  
EARLIER FILING DATE: 1997-08-29  
NUMBER OF SEQ ID NOS: 128  
SOFTWARE: Patent Ver. 2.0  
SEQ ID NO 63  
LENGTH: 145  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (145)  
OTHER INFORMATION: Xaa equals stop translation  
US-09-257-179-63

Alignment Scores:  
Pred. No.: 0.153 Length: 145  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9  
DB:

US-09-705-500a-1 (1-503) x US-09-257-179-63 (1-145)

QY 142 CTGCAAGATGATTCGGGGCTGACCTAGACCACTTGATTCCTCTTGATTTG 201  
|||:|||||  
DB 34 LeuylsthraspYrlysaenProileaspGln-----Cysaenthr 47  
|||:|||||  
QY 202 -----GTGCACCTTGACATTTTGTGCCAT---TATATTGCATTATGATTTA 249  
|||:|||||  
DB 48 LeuasnProleuValleuProgluYrleuIlehisAlaPheheCysValMetPheleu 67  
|||:|||||  
QY 250 TAAATTAATGATATTAGTTTGGCTGAGTACTGGAATAAAC-----AGT 297  
|||:|||||  
DB 68 -----CysAlaIaIaGlutPleuthrleuGlyLeuasnMetProleuLeuAla 83  
|||:|||||  
QY 298 GAGCATATCTGG---TATATGTC----- 318  
|||:|||||  
DB 84 TyhisIleTyrPargYrMetSerArgProValMetSerGlyProgluYrleuYrAspPro 103  
|||:|||||  
QY 319 TTATTATTGTAAATTACATTTTAACTCCATGTCATATATAAGTTATGAACATAT 378  
|||:|||||  
DB 104 ThrThrIleMetasnAlaAspIleleuAlaItyrCysGlnIySglInduIyTrrp----- 120  
|||:|||||  
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGGCTTATTTT 420  
|||:|||||  
DB 121 -----CysIySleuAlaPheYrleuLeuAlaPhe 130  
|||:|||||

#### RESULT 10

US-09-823-038A-48  
Sequence 48, Application US/09823038A  
Patent No. 6797271  
GENERAL INFORMATION:  
APPLICANT: Strachan, Lorna  
APPLICANT: Sleeman, Matthew  
APPLICANT: Abernethy, Nevin  
APPLICANT: Onrust, Rene  
APPLICANT: Kumble, Anand  
APPLICANT: Muirson, Greg  
TITLE OF INVENTION: Compositions isolated from Stromal Cells  
FILE REFERENCE: 11000.1037C3  
CURRENT APPLICATION NUMBER: US/09/823,038A  
CURRENT FILING DATE: 2001-07-09  
NUMBER OF SEQ ID NOS: 61  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 48  
LENGTH: 664  
TYPE: PRT  
ORGANISM: Mouse  
US-09-823-038A-48

Alignment Scores:

Pred. No.:	0.293	Length:	664
Score:	74.50	Matches:	39
Percent Similarity:	45.89%	Conservative:	28
Best Local Similarity:	26.71%	Mismatches:	53
Query Match:	8.52%	Indels:	26
DB:	4	Gaps:	8

QY	3	ATATATATATCATCAATACATATATCATCAATACAGAAAGAGAGATTCACAAATTT	62
Db	24	IIeTfclGlyserIrrh-PheLeuTyrLeuLysPheLeuValValITPAlaLeuValLeuLe	43
QY	63	GCTAGTITTTTTGC-----TTCTCTTTCGCCACCCCTACTCCCTCCAAATCCCCCTTAA	116
Db	43	uAlaaspPheValLeuGluLupheArgPheGluTyrLeuTyrPro-----	57
QY	117	CTTCGAAAGTTCGCTCTTGCTTGGCTGCAGAGTATTCGGGGGCTGCATGACCGATT	176
Db	58	-PheTyrPhePheIleArgSerValTyrAspSerPheArgTyrGlnGlyLeu--AlaPh	76
QY	177	TGCATGATCTCTCTCTGTCGATTTGGTTCGACCTTAGACATTTTGTGSCATTAATTTT	236
Db	76	eSerValPhePheValCys-----ValAla-----PheThrSerAsnIleIleCys	91
QY	237	CATTATGCTATTTTAATTTAAATGATATTTAGCTTTTGGCTGCACTACTGCMAATTAACAG	296
Db	91	StenLeuPheIleProIleGln--TriPhePhePheAlaAlaSerIrrTyrValITrPva	110
QY	297	TGAGCATATCTGGTAT-----ATGTCATATTTATTTATGT	328
Db	110	IGlnTyrValTrrHisThrGluArgGlyValCysLeuProThrValaSerLeuITrPlele	130
QY	330	TAAATTACATTTTAAAGCTCCATGTCGATTAATAAGGTTATGAAACATATCATGTGAATGA	388
Db	130	uPheValTyrIleGluAlaAlaIleArgPheLysAspLeuLysAsnPheHis---ValAs	145
QY	390	CAGATGCAAGTATTT	405
Db	149	pLeuCysArgPheProPhe	154

```

RESULT 11
US-09-270-767-46166
; Sequence 46166, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 46166
; LENGTH: 330
; TYPE: PR1
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-46166

```

Alignment Scores:	
Pred. No.:	0.443
Score:	72.50
Percent Similarity:	39.02%
Best Local Similarity:	26.22%
Query Match:	8.20%
DB:	4
Length:	33
Matches:	23
Conservative:	21
Mismatches:	53
Indels:	8
Gaps:	7

QY 397 TGCATGTCATTACCATGATATGTTCTTAAC---CTTTATATGCACATGAGCTTAAA 341  
||||||| || ||||| :||| ||||| :|||

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Db      86  CysIleCysIleTy-ValAlaAsnIleShiSsnThrIleCysMethCisIlePole--- 104
Qy      340  AAATGTAATTTAAACATAAATAATATGACATATACGAGATATGCTACAGCTTATTCCAGTAC 281
Db      105  -----***PheThrSerAsnArg--IleGlnCysIleIleMetAsn 117
Qy      280  TCAGCCAAAACCTAATATATCATTTTAATTTAATTAATCATATATGCAATATTAATGGACA 221
Db      118  ArgAlaIleGlnIleAsnSerIle-----Thr-Asn***AsnGlyIleAsnIy 132
Qy      220  AAAATGTTCTAAAGTGCACCAACATATACAGAGAAAGATCATGCAACTGGTCTTAGGTTCAG 161
Db      132  sIySGlnAsnSerAsnIySGlnThrThrThrGlnIleAsnAsnIySGlnIleArgIleAs 152
Qy      160  CCCCAGATCATCTCTGCAGCAACAC-----AAGACGAGAGCTTTGAGAGTTTAAGGGG 107
Db      152  nAsnIySlySlySleu-IleIyShiThrGlnIySerySGlnIleIySerySerGlyG 172
Qy      106  AATTGGAGGGA-----GTAGGCTGGGGGAAAGACAGACAAAAA 68
Db      172  IyCysGlyIyGlnThrThrIySGlnSerGlnLeuArgTIPGlyIleSile**AsnIyS 192
Qy      67  CTAGCAACACTTGTGAGAACTGCT----- 45
Db      192  erSerAsnIySeryIshIserIyS****Leu*****ArgIySlyIySlySlySly 212
Qy      44  -----TCTTCTGATGATGTAGA-----TATATGATTTGTA 14
Db      212  hrAspArgIyShrAlaIyS***PheCysIleValArgGArgAsnAsnIyIySlyTyAsnI 232
Qy      13  GATACATA 6
Db      232  euTyIyIleu 234

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```

RESULT 12
US-09-270-767-34960
; Sequence 34960, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 34960
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-34960

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Alignment Scores:	
Pred. No.:	0.622
Score:	71.50
Percent Similarity:	40.00%
Best Local Similarity:	25.52%
Query Match:	8.18%
DB:	4
	7
Length:	35
Matches:	37
Conservative:	21
Mismatches:	50
Indels:	37
Gaps:	7

US-09-705-500A-1 (1-503) \* US-09-270-767-34960 (1-353)

QY 1 CTAATATGATCTCAATATATATCTCACATATACAGAAAGACAGTTCTCACAAATG 60  
||| ||| :|||:||||:|||||P|||||  
Db 226 LeuLeuProTyTyValPheIleHisValTyIleHisProLeuSmaIaLeuThrAsn 245  
||| ||| :|||:||||:|||||P|||||  
QY 61 TTTG-----CTAGTTTTTGTCTCTCTTTCCCAACCTACTCTCCCAAT----- 105  
||| ||| :|||:||||:|||||P|||||  
Db 246 LeuTyTyIreLeuGcAlaSerThrSerSerSerSerProIaAsn\*\*\*ProIhr 265  
||| ||| :|||:||||:|||||P|||||  
QY 106 TCCCCCTTAACCTTCCAAAGCTTGCTCTTGtGTTTGTGcAGAGTGAATTGGGGGGCTGAC 165



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Db      266  ThrProIleSerPheValCysValThrLeuCysTrpLeu-----SerAlaGln 281
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Qy      166  CTAGACGAGTTTGCATGATCTTCTCTGTGATTGGTTGCACCTTAGACATTTTGTGC 225
               |||||
Db      282  LeuAspLeuThrAlaIlePheLeuSerValIleVal-----294
               |||||
Qy      226  CATTATATTGCATTTAGTATTATATTAATGATATTAGTTTGGCTGAGTACT 285
               ::|||::|
Db      295  PhePheValIlePhePheArgAspPheAsnGluPhe-----PhePheAlaValVal 312
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Qy      286  GGAATTAACAGTGCATATCTGTATATGTCATTATTATTTGTTAAATTACATTTTAA 345
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Db      313  LeuValSerSerGlnIys**TyrTyr-----LeuPhePheValIleLeuPhePhe--- 329
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               ::|||::|
Db      330  -----CysPheSerPhe 333
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Qy      406  TATTGCTTATTTT 420
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Db      334  LeuValPheIlePhe 338

RESULT 13
US-09-270-767-50177
; Sequence 50177, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50177
; LENGTH: 353
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50177

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Alignment Scores:
Pred. No.: 0.622 Length: 353
Score: 71.50 Matches: 37
Percent Similarity: 40.00% Conservative: 21
Best Local Similarity: 25.52% Mismatches: 50
Query Match: 8.18% Indels: 37
DB: 4 Gaps: 7
US-09-705-500a-1 (1-503) x US-09-270-767-50177 (1-353)

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Qy      1  CTATATATGATCTACATATACATATATCTACATATCAAGAAAGACAGTTCTCACATG 60
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Db      226  LeuLeuProTyrTyrValPheIleHisValTyrIleHisProLeuAsnIleLeuThrAsn 245
               |||||
Qy      61  TTG-----CTAGTTTGTGCTCTCTTCCCAACCTTACCTCCCTTCAT-----105
               |||||
Db      246  LeuTyrTyrLeuLeuCysAlaSerThrSerSerSerSerProAlaAsn**ProThr 265
               |||||
Qy      106  TCCCCCTTAACCTCCAAAGCTTGCTGTGATGTTGTGAGAGTGATGGGGGCTGAC 165
               |||||
Db      266  ThrProIleSerPheValCysValThrLeuCysTrpLeu-----SerAlaGln 281
               |||||
Qy      166  CTAGACGAGTTTGCATGATCTTCTCTGTGATTGGTTGCACCTTAGACATTTTGTGC 225
               |||||
Db      282  LeuAspLeuThrAlaIlePheLeuSerValIleVal-----294
               |||||
Qy      226  CATTATATTGCATTTAGTATTATATTAATGATATTAGTTTGGCTGAGTACT 285
               ::|||::|
Db      295  PhePheValIlePhePheArgAspPheAsnGluPhe-----PhePheAlaValVal 312
               ::|||::|

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Qy      286  GGAATTAACAGTGCATATCTGTATATGTCATTATTATTTGTTAAATTACATTTTAA 345
               ::|||::|
Db      313  LeuValSerSerGlnIys**TyrTyr-----LeuPhePheValIleLeuPhePhe--- 329
               ::|||::|
Qy      346  GCTCCATGTGCATATTAAGGTTATGAACAATATCATGATGATGACAGATGCAAGTTATT 405
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Db      330  -----CysPheSerPhe 333
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Qy      406  TATTGCTTATTTT 420
               ::|||
Db      334  LeuValPheIlePhe 338

RESULT 14
US-09-248-796A-27951
; Sequence 27951, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstein et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 27951
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-27951

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Alignment Scores:
Pred. No.: 0.493 Length: 63
Score: 70.50 Matches: 17
Percent Similarity: 52.94% Conservative: 10
Best Local Similarity: 33.33% Mismatches: 19
Query Match: 8.07% Indels: 5
DB: 4 Gaps: 2
US-09-705-500a-1 (1-503) x US-09-248-796A-27951 (1-63)

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Qy      19  TACATATATCTTACATATACAG-----AAAGACAGTTCTCACATGTTG--- 63
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Db      8  TyrIleLeuLeuTyrIleIleValIleProProAsnHisAlaThrAlaSerIleLeuHis 27
               |||||
Qy      64  CTAGTTTGTGCTCTCTTCCCAACCTTACCTCCCTTAACTTCCAA 123
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Db      28  SerValPheCysPheThrTyrSerHisAsnIleProIysAsnSerProIleHisAspHis 47
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Qy      124  AGCTTGTCTGTGTGTTCTGCTGACAGTATTCG 156
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Db      48  AspPheGluValValPhePheSerThrGlySer 58
               ::|||

RESULT 15
US-09-134-000C-5472
; Sequence 5472, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5472
; LENGTH: 405

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! TYPE: PRT  
! ORGANISM: Enterococcus faecalis  
US-09-134-000C-5472

## Alignment Scores:

Pred. No.:	0.895	Length:	405
Score:	70.50	Matches:	31
Percent Similarity:	40.68%	Conservative:	17
Best Local Similarity:	26.27%	Mismatches:	46
Query Match:	8.07%	Indels:	24
DB:	4	Gaps:	4

US-09-705-500a-1 (1-503) x US-09-134-000C-5472 (1-405)

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Db 7 AsnProHisMetIleProIYrAsnAlaProIYrTyrPheValLeuLeuIleAla 26
QY 139 TTGCTGACAGATGATTCGGGGCTGACCTAGACCAAGTTGCATGATTCCTCTTGAT 198
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 27 LeuLeuPro-MetIleLeuThrLeuAlaIleIYsGlyThrArg----- 40
QY 199 TTGGTTGCACCTTAGACATTTTGTGCCATTATTTGCATTTATGTATTTATTTAA 258
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 41 -TTPProIYrGlnThrLeuValThrLeuValPheLeu-TyrIle----- 55
QY 259 TGAATTATTAGATTTTGGCTGACTGCAATAAACAAGTACATCTGTATATGCA 318
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 56 -----SerPheGlyGlyGlnPheTrpGlnGlnIYValAlaLeuIleValIYValI 73
QY 319 TTATTTATTTGTTAAATTACATTTTAACTCCATGTCATATATAAGTTATGAAACATAT 378
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 73 le-TyrGlnThrLeuLeuThrP-----GlyTyrAlaAlaIYr 85
QY 379 CATGTATATGACAGATGCAAG--TTATTTATTTGCTTATTTTATA 423
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 ArgIYsAsnIYsAsnAlaGlyTTPValPheTyrLeuAlaValPheLeu 101
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Search completed: November 22, 2004, 17:50:03  
Job time : 24.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: November 22, 2004, 17:42:57 ; Search time 271.5 Seconds

(without alignments)  
1312.163 Million cell updates/sec

Title: US-09-705-500A-1  
Perfect score: 874  
Sequence: 1 cctacatctctctacacata.....tataaagtgctacgtttta 503

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1570615 seqs, 354127592 residues

Total number of hits satisfying chosen parameters: 3141230

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-TRANS=human40.cdi -LIST=45 -DOCCALIGN=200 -THR SCORE=Pct -THR MAX=100  
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-LONGLOG -DEV\_TIMEOUT=120 -WARN\_TIME=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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Published Applications AA: \*  
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18: /cgn2\_6/prodata/2/pubppa/US11\_NEW\_PUB.pep: \*  
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20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### ALIGNMENTS

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1	78.5	9.0	291	14	US-10-017-161-2388	Sequence 2388, Ap
2	78.5	9.0	291	14	US-10-292-798-2030	Sequence 2030, Ap
3	78	8.9	338	14	US-10-017-161-2058	Sequence 2058, Ap
4	78	8.9	338	14	US-10-292-798-1704	Sequence 1704, Ap
5	75.5	8.6	298	14	US-10-017-161-2194	Sequence 2194, Ap
6	75.5	8.6	298	14	US-10-292-798-1840	Sequence 1840, Ap
7	75.5	8.5	471	15	US-10-108-2604-4551	Sequence 4551, Ap
8	75	8.6	109	15	US-10-424-599-189266	Sequence 189266, Ap
9	75	8.6	142	9	US-09-765-205-2	Sequence 2, Appl1
10	75	8.6	144	9	US-09-978-295A-322	Sequence 322, App
11	75	8.6	144	9	US-09-736-457-327	Sequence 327, App
12	75	8.6	144	9	US-09-978-657-322	Sequence 322, App
13	75	8.6	144	9	US-09-902-941-327	Sequence 327, App
14	75	8.6	144	9	US-09-978-182A-322	Sequence 322, App
15	75	8.6	144	9	US-09-999-832A-322	Sequence 322, App
16	75	8.6	144	9	US-09-849-626-327	Sequence 327, App
17	75	8.6	144	9	US-09-978-189-322	Sequence 322, App
18	75	8.6	144	10	US-09-978-608A-322	Sequence 322, App
19	75	8.6	144	10	US-09-978-585A-322	Sequence 322, App
20	75	8.6	144	10	US-09-978-191A-322	Sequence 322, App
21	75	8.6	144	10	US-09-978-403A-322	Sequence 322, App
22	75	8.6	144	10	US-09-978-564A-322	Sequence 322, App
23	75	8.6	144	10	US-09-999-833A-322	Sequence 322, App
24	75	8.6	144	10	US-09-981-915A-322	Sequence 322, App
25	75	8.6	144	10	US-09-978-824-322	Sequence 322, App
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29	75	8.6	144	10	US-09-978-193A-322	Sequence 322, App
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42	75	8.6	144	10	US-09-978-544A-322	Sequence 322, App
43	75	8.6	144	10	US-09-978-665A-322	Sequence 322, App
44	75	8.6	144	10	US-09-978-802A-322	Sequence 322, App
45	75	8.6	144	11	US-09-999-831A-322	Sequence 322, App

RESULT 1  
US-10-017-161-2388  
; Sequence 2388, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUMA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: ABURATANI, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2388  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-2388

Alignment Scores:  
 Pred. No.: 1.5 Length: 291  
 Score: 78.50 Matches: 31  
 Percent Similarity: 33.56% Conservative: 19  
 Best Local Similarity: 20.81% Mismatches: 40  
 Query Match: 8.98% Indels: 59  
 DB: 14 Gaps: 8

US-09-705-500a-1 (1-503) x US-10-017-161-2388 (1-291)

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QY 56 CAATGTGCTAGTTTTTGGCTCTCTTCCGCCACCTACTCCCTCAATTCCTCCCTTAA 115
DB 69 ThrCys-----ThrCys-----ThrCys-----ThrCys-----ThrCys 70
QY 116 ACTTCGAAAGCTTCGTTGTTGTTGCTGCAGAGTATTCGGGGCTGACCTAGACCACT 175
DB 71 -----ValHisMetCysMetCys-----ThrCys 78
QY 176 TTGCAT-----GATTCCTCTCTGATTTGATTTGATTCGATTTAGA 214
DB 79 ValHisValCysMetCysAlaCysValHisValArgMetCysValTyMetHisThrArg 98
QY 215 CATTTTGGCCATTAATTTGGCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 274
DB 99 ---ThrCysValTyrlle-----CysThrTyThr-----ThrCys 107
QY 275 GGGTGAAGTACTGAAATTAACAGTACAGTATCTGTATGATGATTTATTTATTTAAAT 334
DB 108 -----HisValTyrlleValCysileCysThrTyThrArgValHis 121
QY 335 TACATTTTAAAGCTCCATGTCATATGAAGTTATGAACATATCATGTAATGACAGAT 394
DB 122 CysValTyThr-----MetHisileTyThrCysValHisValCysileCysThrTy 138
QY 395 GCAAGTATTTTATTTGCTTATTTTA 421
DB 139 ThrArgValTyMetCysValTyMet 147

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RESULT 2  
 US-10-292-798-2030  
 ; Sequence 2030, Application US/10292798  
 ; Publication No. US2003023583A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUMA, MAKIKO  
 ; APPLICANT: ASAI, KIYOSHI  
 ; APPLICANT: AKIYAMA, YUTAKA  
 ; APPLICANT: ASURATANI, HIROYUKI  
 ; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
 ; FILE REFERENCE: 084335/166  
 ; CURRENT APPLICATION NUMBER: US/10/292,798  
 ; CURRENT FILING DATE: 2002-11-13  
 ; PRIOR APPLICATION NUMBER: 10/017,161  
 ; PRIOR FILING DATE: 2001-12-18  
 ; PRIOR APPLICATION NUMBER: JP 2001-246789  
 ; PRIOR FILING DATE: 2001-06-18  
 ; NUMBER OF SEQ ID NOS: 2070  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2030  
 ; LENGTH: 291  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-292-798-2030

Alignment Scores:  
 Pred. No.: 1.5 Length: 291  
 Score: 78.50 Matches: 31  
 Percent Similarity: 33.56% Conservative: 19  
 Best Local Similarity: 20.81% Mismatches: 40

Query Match: 8.98% Indels: 59  
 DB: 14 Gaps: 8

US-09-705-500a-1 (1-503) x US-10-292-798-2030 (1-291)

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QY 2 TATATGATCTACATACATA-----TATATGATCTACATACAGAAAGAGAGCTTCTCA 55
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QY 56 CAATGTGCTAGTTTTTGGCTCTCTTCCGCCACCTACTCCCTCAATTCCTCCCTTAA 115
DB 69 ThrCys-----ThrCys-----ThrCys-----ThrCys-----ThrCys 70
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DB 71 -----ValHisMetCysMetCys-----ThrCys 78
QY 176 TTGCAT-----GATTCCTCTCTGATTTGATTTGATTCGATTTAGA 214
DB 79 ValHisValCysMetCysAlaCysValHisValArgMetCysValTyMetHisThrArg 98
QY 215 CATTTTGGCCATTAATTTGGCATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 274
DB 99 ---ThrCysValTyrlle-----CysThrTyThr-----ThrCys 107
QY 275 GGGTGAAGTACTGAAATTAACAGTACAGTATCTGTATGATGATTTATTTATTTAAAT 334
DB 108 -----HisValTyrlleValCysileCysThrTyThrArgValHis 121
QY 335 TACATTTTAAAGCTCCATGTCATATGAAGTTATGAACATATCATGTAATGACAGAT 394
DB 122 CysValTyThr-----MetHisileTyThrCysValHisValCysileCysThrTy 138
QY 395 GCAAGTATTTTATTTGCTTATTTTA 421
DB 139 ThrArgValTyMetCysValTyMet 147

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RESULT 3  
 US-10-017-161-2058  
 ; Sequence 2058, Application US/10017161  
 ; Publication No. US2003014366A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: SUMA, MAKIKO  
 ; APPLICANT: ASAI, KIYOSHI  
 ; APPLICANT: AKIYAMA, YUTAKA  
 ; APPLICANT: ASURATANI, HIROYUKI  
 ; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
 ; FILE REFERENCE: 084335/0152  
 ; CURRENT APPLICATION NUMBER: US/10/017,161  
 ; CURRENT FILING DATE: 2002-12-18  
 ; PRIOR APPLICATION NUMBER: JP 2001/246789  
 ; PRIOR FILING DATE: 2001-06-18  
 ; NUMBER OF SEQ ID NOS: 2430  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 2058  
 ; LENGTH: 338  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-017-161-2058

Alignment Scores:  
 Pred. No.: 1.77 Length: 338  
 Score: 78.00 Matches: 32  
 Percent Similarity: 33.12% Conservative: 19  
 Best Local Similarity: 20.78% Mismatches: 41  
 Query Match: 8.92% Indels: 62  
 DB: 14 Gaps: 7

US-09-705-500a-1 (1-503) x US-10-017-161-2058 (1-338)  
 QY 2 TATATGATCTACATACATAATATATACATACAGAAAGAGAGCTTCAATGT 61  
 DB 228 TyrValCysValTyrlleHisThrileTyThr----- 238

QY 62 TGCTAGTTTTGCTTCTCTTTCCACCACCTACCTCCATTCACATTCGCCCTTAACCTTCC 121  
Db 238 ----- 238  
QY 122 AAAGCTTCGTTGCTTGTCTGTCGACAGATGATTCGGGGGCTGACCTAGACCAAGTTGCAT 181  
Db 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValIyTrHis 255  
QY 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValIyTrHis 255  
Db 182 GATTCT-----TCCTTGATTTGGTTGCAC 208  
QY 256 ThnHisTyThrHisTyValIyTrThrHisThrIleTyThrLeuCysValIyTrHis 275  
Db 209 TTTAGACATTT--TGTCGC--ATTATATTGCATTATGATTATTAATTAATGAT 262  
Db 276 TyArgHisTyValCysThrHisThrIleTyThrLeuCysValIyTr----- 291  
QY 263 ATTAGGTTTTGGCTGAGTACGAAATGAACAGTAGCATACCTGATTA--TGTCAT 319  
Db 292 -----ThnHisThrIleTyThrLeuTyThrHis 301  
QY 320 TATTATGTTAAATTACATTTTAACTCCATGTCATATGAAGTTATGAACATATC 379  
Db 302 ThrIleTyThrLeuTyThrIle-----LeuHisIleTyThrIleValIyMetTyThrIle 319  
QY 380 ATGCTAATGACAGATGCAAGTTATTTATTTGCTTATTTTA 421  
Db 320 CysValIyTrThrHisAsnValIyThrIlePheThrSerPheMet 333  
RESULT 4  
US-10-292-798-1704  
; Sequence 1704, Application US/10292798  
; Publication No. US2003025833A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURANT, HIROYUKI  
; TITLE OF INVENTION: GUANOSINE TRIPHOSPHATE-BINDING PROTEIN COUPLED RECEPTORS  
; FILE REFERENCE: 084335/166  
; CURRENT APPLICATION NUMBER: US/10/292, 798  
; CURRENT FILING DATE: 2002-11-13  
; PRIOR APPLICATION NUMBER: 10/017,161  
; PRIOR FILING DATE: 2001-12-18  
; PRIOR APPLICATION NUMBER: JP 2001-246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2070  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1704  
; LENGTH: 338  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-292-798-1704  
Alignment Scores:  
Pred. No.: 1.77 Length: 338  
Score: 78.00 Matches: 32  
Percent Similarity: 33.12% Conservative: 19  
Best Local Similarity: 20.78% Mismatches: 41  
Query Match: 8.92% Indels: 62  
DB: 14 Gaps: 7  
US-09-705-500a-1 (1-503) x US-10-292-798-1704 (1-338)  
QY 2 TATATGATCTACATACATATATCTACATACAGAAAGAGAGTTCTCACATGT 61  
Db 228 TyValCysValIyThrHisThrIleTyThr----- 238  
QY 62 TGCTAGTTTTGCTTCTCTTCCGCCACCTACTCCCTCCATTCGCCCTTAACCTCC 121  
Db 238 ----- 238  
QY 122 AAAGCTTCGTTGCTTGTCTGTCGACAGATGATTCGGGGGCTGACCTAGACCAAGTTGCAT 181

Db 239 -----MetCysValCysAlaIyTrThrHisThrIleTyThrLeuCysValIyTrHis 255  
QY 182 GATTCT-----TCCTTGATTTGGTTGCAC 208  
Db 256 ThnHisTyThrHisTyValIyTrThrHisThrIleTyThrLeuCysValIyTrHis 275  
QY 209 TTTAGACATTT--TGTCGC--ATTATATTGCATTATGATTATTAATTAATGAT 262  
Db 276 TyArgHisTyValCysThrHisThrIleTyThrLeuCysValIyTr----- 291  
QY 263 ATTAGGTTTTGGCTGAGTACGAAATGAACAGTAGCATACCTGATTA--TGTCAT 319  
Db 292 -----ThnHisThrIleTyThrLeuTyThrHis 301  
QY 320 TATTATGTTAAATTACATTTTAACTCCATGTCATATGAAGTTATGAACATATC 379  
Db 302 ThrIleTyThrLeuTyThrIle-----LeuHisIleTyThrIleValIyMetTyThrIle 319  
QY 380 ATGCTAATGACAGATGCAAGTTATTTATTTGCTTATTTTA 421  
Db 320 CysValIyTrThrHisAsnValIyThrIlePheThrSerPheMet 333  
RESULT 5  
US-10-017-161-2194  
; Sequence 2194, Application US/10017161  
; Publication No. US20030143668A1  
; GENERAL INFORMATION:  
; APPLICANT: SUWA, MAKIKO  
; APPLICANT: ASAI, KIYOSHI  
; APPLICANT: AKIYAMA, YUTAKA  
; APPLICANT: AUBURANT, HIROYUKI  
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS  
; FILE REFERENCE: 084335/0152  
; CURRENT APPLICATION NUMBER: US/10/017,161  
; CURRENT FILING DATE: 2002-12-18  
; PRIOR APPLICATION NUMBER: JP 2001/246789  
; PRIOR FILING DATE: 2001-06-18  
; NUMBER OF SEQ ID NOS: 2430  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2194  
; LENGTH: 298  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-017-161-2194  
Alignment Scores:  
Pred. No.: 3.58 Length: 298  
Score: 75.50 Matches: 36  
Percent Similarity: 36.84% Conservative: 20  
Best Local Similarity: 23.68% Mismatches: 37  
Query Match: 8.64% Indels: 59  
DB: 14 Gaps: 6  
US-09-705-500a-1 (1-503) x US-10-017-161-2194 (1-298)  
QY 49 GTTCTCACATGTTGCTAGTTTGTCTCTTTCCTTCCACCACCTACTCCCTCCATTC 108  
Db 74 ValLeuSerCysPheProValPheLeuLeuSerPhe----- 85  
QY 109 CCTTAACTTCCAAAGTTGCTTGTGTTGTGTCAGAGATGATTCGGGGGCTGACCTA 168  
Db 86 -----PheLeuSerPheLeuSerCysLeuLeu----- 94  
QY 169 GACCAAGTTGATGATCTCTCTTGATTTGGTTGCACATTAGACATTTTGGCAT 228  
Db 95 -----SerCysLeuLeuAlaCysPheArgAlaPheLeuLeuSer 107  
QY 229 TATATGCAATTATGATTTTAAATTATTAATGATATTAGTTTGG----- 276  
Db 108 -----CysPheLeuPheLeuSerPhe-----PheLeuSerPheTyCysPhePheLeu 123  
QY 277 -----CTGAGTACTGCAATTAACAGTACGATATCTATCTGATATATG 315



LENGTH: 109  
TYPE: PRT  
ORGANISM: Glycine max  
FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_141923C.1.pdp  
US-10-424-599-189266

Alignment Scores:  
Pred. No.: 3.51 Length: 109  
Score: 75.00 Matches: 24  
Percent Similarity: 42.53% Conservative: 13  
Best Local Similarity: 27.59% Mismatches: 36  
Query Match: 8.58% Indels: 14  
DB: 15 Gaps: 2

US-09-705-500a-1 (1-503) x US-10-424-599-189266 (1-109)

QY 73 TGCTTCCTCTTC-----CCGCACCTACTCCC 99  
Db 10 CysAlaSerPheAsnSerLeuHisIlyMetGlyTyrValSerGlnHisLeuProPro 29  
QY 100 TCCAAATTCCTCCCTTAACTTCCAAAGCTTC-----GTCTTGCTTGTCTGACAGT 150  
Db 30 ThPheSerProLeuHisPheSerValPheThrPheSerIleTyrThrLeuLeuHisHis 49  
QY 151 GATTCGGGGGCTGACCTGACGACAGCTTGCATGATTCCTCTGCTGATTTGGTGCACCT 210  
Db 50 HisValValPheAspIleThrGlnPheSerLeuValPheSerCysLeuAlaLeuSerLeu 69  
QY 211 TAGACATTTTGTCCCATTTATTTGTCATTTATTTAATTAATGATTTAGT 270  
Db 70 CysPhePheValCysLeuTyrPhePheGlnLeuPheHisLeuSerLeuHisLeuGln 89  
QY 271 TTTTGCTGAGTACTGCAATA 291  
Db 90 ValTyrPasnGlnThrAsnLeu 96

RESULT 9  
US-09-765-205-2  
Sequence 2, Application US/09765205  
Patent No. US20020034800A1  
GENERAL INFORMATION:  
APPLICANT: Cao, Li  
TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES  
FILE REFERENCE: 1458, 004/200130, 449  
CURRENT APPLICATION NUMBER: US/09/765, 205  
CURRENT FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: US/09/212, 440  
PRIOR FILING DATE: 1998-12-16  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 142  
TYPE: PRT  
ORGANISM: human  
US-09-765-205-2

Alignment Scores:  
Pred. No.: 3.67 Length: 142  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: 9 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-765-205-2 (1-142)

QY 142 CTGCAGAGTATTCGGGGGCTGACCTAGACAGTTGTCATGATTTCTTCTGTGATTTG 201  
Db 32 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 45  
QY 202 -----GTTCACCTTAGACATTTTGTGCCAT---TATATTTGCATTAAGTATTA 249

Db 46 LeuAsnProLeuValLeuProGlnTyrLeuIleHisAlaPhePheCysValMetPheLeu 65  
QY 250 TAATTTAATGATATTTAGTTTGGCTGAGTACTGAGATTAAC-----AGT 297  
Db 66 -----CysAlaAlaGlnTyrPheThrLeuGlnLeuAsnMetProLeuLeuAla 81  
QY 298 GAGCATATCTGG---TATATGTCA----- 318  
Db 82 TyrHisIleTyrPasnGlyTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 101  
QY 319 TTATTTATGTTAATTAATTCATTTTAAAGCTCCATGTCATTAAGGTTATGAACAATAT 378  
Db 102 ThrThrIleLeuAsnAlaAspIleLeuAlaTyrCysGlnLysGlnGlyTyr----- 118  
QY 379 CATGGTAATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420  
Db 119 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 128

RESULT 10  
US-09-978-295A-322  
Sequence 322, Application US/0978295A  
Patent No. US20020156006A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fond, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gottlieb, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C11  
CURRENT APPLICATION NUMBER: US/09/978, 295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/074450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11

PRIOR APPLICATION NUMBER:	60/077791
PRIOR FILING DATE:	1998-03-12
PRIOR APPLICATION NUMBER:	60/078004
PRIOR FILING DATE:	1998-03-13
PRIOR APPLICATION NUMBER:	60/078886
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078936
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078910
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/078939
PRIOR FILING DATE:	1998-03-20
PRIOR APPLICATION NUMBER:	60/079294
PRIOR FILING DATE:	1998-03-25
PRIOR APPLICATION NUMBER:	60/079656
PRIOR FILING DATE:	1998-03-26
PRIOR APPLICATION NUMBER:	60/079664
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079669
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079663
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079788
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079786
PRIOR FILING DATE:	1998-03-27
PRIOR APPLICATION NUMBER:	60/079920
PRIOR FILING DATE:	1998-03-30
PRIOR APPLICATION NUMBER:	60/079923
PRIOR FILING DATE:	1998-03-30
PRIOR APPLICATION NUMBER:	60/080105
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/080107
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/080165
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/080194
PRIOR FILING DATE:	1998-03-31
PRIOR APPLICATION NUMBER:	60/080327
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/080328
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/080333
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/080334
PRIOR FILING DATE:	1998-04-01
PRIOR APPLICATION NUMBER:	60/081070
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081049
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081071
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081195
PRIOR FILING DATE:	1998-04-08
PRIOR APPLICATION NUMBER:	60/081203
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081229
PRIOR FILING DATE:	1998-04-09
PRIOR APPLICATION NUMBER:	60/081955
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081817
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081819
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081952
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/081836
PRIOR FILING DATE:	1998-04-15
PRIOR APPLICATION NUMBER:	60/082568
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082565
PRIOR FILING DATE:	1998-04-21
PRIOR APPLICATION NUMBER:	60/082704



PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	3.68	Length:	144
Score:	75.00	Matches:	33
Percent Similarity:	41.74%	Conservative:	15
Best Local Similarity:	28.70%	Mismatches:	27
Query Match:	9	Indels:	40
DB:	9	Gaps:	9

US-09-705-500a-1 (1-503) x US-09-978-295a-322 (1-144)

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QY 142 CTGAGAGTATTCGGGGGCTGACCTAGACGATTGTCATGATTTCTCTGTGATTG 201
DB 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTTGACCTTTAGACATTTTGTGCCAT---TATATTGCAATTATGATTTA 249
DB 48 LeuAsnProLeuValLeuProGlnTyrLeuIleHisAlaPhePheCysValMetPheLeu 67
QY 250 TAAATTAATGATATTAGGTTTGGCTGAGTACTGCAATAAAC-----AGT 297
DB 68 -----CysAlaAlaGlnTyrPheThrLeuGlnLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTGG---TATATGTCA----- 318
DB 84 TyrHisIleTyrPargTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTAATTCATTTTAACTCCATGTCATATAAGTTATGAACATAT 378
DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnTyrsglnTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGCTTATTTT 420
DB 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
```

## RESULT 11

US-09-736-457-327  
Sequence 327, Application US/09736457  
Patent No. US20020168637A1  
GENERAL INFORMATION:  
APPLICANT: Wang, Tongtong  
APPLICANT: Bangur, Chaitanya S.  
APPLICANT: Lodes, Michael A.  
APPLICANT: Fanger, Gary  
APPLICANT: Vedvick, Tom  
APPLICANT: Carter, Darrick  
APPLICANT: Retter, Marc  
APPLICANT: Mannion, Jane  
APPLICANT: Fan, Liqun  
APPLICANT: Wang, Liqun  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
FILE REFERENCE: 210121.478C15  
CURRENT APPLICATION NUMBER: US/09/736,457  
CURRENT FILING DATE: 2000-12-13  
NUMBER OF SEQ ID NOS: 1864  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 327  
LENGTH: 144  
TYPE: PRN  
ORGANISM: Homo sapiens  
US-09-736-457-327

## Alignment Scores:

Pred. No.:	3.68	Length:	144
Score:	75.00	Matches:	33
Percent Similarity:	41.74%	Conservative:	15
Best Local Similarity:	28.70%	Mismatches:	27
Query Match:	9	Indels:	40
DB:	9	Gaps:	9

US-09-705-500a-1 (1-503) x US-09-736-457-327 (1-144)

```
QY 142 CTGAGAGTATTCGGGGGCTGACCTAGACGATTGTCATGATTTCTCTGTGATTG 201
DB 34 LeuLysThrAspTyrLysAsnProIleAspGln-----CysAsnThr 47
QY 202 -----GTTGACCTTTAGACATTTTGTGCCAT---TATATTGCAATTATGATTTA 249
DB 48 LeuAsnProLeuValLeuProGlnTyrLeuIleHisAlaPhePheCysValMetPheLeu 67
QY 250 TAAATTAATGATATTAGGTTTGGCTGAGTACTGCAATAAAC-----AGT 297
DB 68 -----CysAlaAlaGlnTyrPheThrLeuGlnLeuAsnMetProLeuLeuAla 83
QY 298 GAGCATATCTGG---TATATGTCA----- 318
DB 84 TyrHisIleTyrPargTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTATTGTTAAATTAATTCATTTTAACTCCATGTCATATAAGTTATGAACATAT 378
DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnTyrsglnTyrP----- 120
QY 379 CATGTAATGACAGATGCAAGTTA---TTTATTGCTTATTTT 420
DB 121 -----CysLysLeuAlaPheTyrLeuLeuAlaPhe 130
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## RESULT 12

US-09-978-697-322  
Sequence 322, Application US/09978697  
Patent No. US20020169284A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P26302P127  
CURRENT APPLICATION NUMBER: US/09/978,697  
CURRENT FILING DATE: 2001-10-16  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450

[illegible]

PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085573  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085704  
PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: 9 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-978-697-322 (1-144)

QY 142 CTGCAGATGATTCGGGGCTGACCTAGACCAAGTTGATGATTTCTCTGTGATTTG 201  
|||:|||||  
DB 34 LeuLYSThrAspIYrLYSAsnProIleAspGln-----CysAsnThr 47  
QY 202 -----GTGACCTTTAGACATTTTGTGGCAT--TATATTGCATTTATGATTTA 249  
|||:|||||  
DB 48 LeuAsnProIleValLeuProGluTYrLeuIleHisAlaPhePheCysValMetPheLeu 67  
QY 250 TATTTTAAATGATTTAGGTTTGTGGCTGAGTACTGAAATAAC-----AGT 297  
|||:|||||  
DB 68 -----CysAlaAlaGluTrpLeuThrLeuGluLeuAsnMetProIleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
|||:|||||  
DB 84 TYRHisIleTrpArgTYrMetSerArgProValMetSerGlyProGlyLeuTYrAspPro 103  
QY 319 TTTATTATGTTAAATTACATTTTAAAGTCATGTCATATAAGGTATGAAACATAT 378  
|||:|||||  
DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTYrCysGlnLYSGluGlyTrp----- 120  
QY 379 CATGTTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420  
|||:|||||  
DB 121 -----CysLYSLeuAlaPheTYrLeuLeuAlaPhe 130

RESULT 13

US-09-902-941-327  
Sequence 327, Application US/09902941  
Patent No. US20020172952A1

GENERAL INFORMATION:  
APPLICANT: Henderson, Robert A.

APPLICANT: Wang, Tongcong

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Johnson, Jeffrey C.

APPLICANT: Reiter, Marc W.

APPLICANT: Marnierakis, Margarita

APPLICANT: Carter, Derrick

APPLICANT: Fanger, Gary R.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Bangur, Chaitanya S.

APPLICANT: McNabb, Andria

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

FILE REFERENCE: 210121.478C17

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 2002

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 327

LENGTH: 144

TYPE: PRT

ORGANISM: Homo sapiens

US-09-902-941-327

Alignment Scores:

Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
DB: 9 Gaps: 9

US-09-705-500A-1 (1-503) x US-09-902-941-327 (1-144)

QY 142 CTGCAGATGATTCGGGGCTGACCTAGACCAAGTTGATGATTTCTCTGTGATTTG 201  
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DB 34 LeuLYSThrAspIYrLYSAsnProIleAspGln-----CysAsnThr 47  
QY 202 -----GTGACCTTTAGACATTTTGTGGCAT--TATATTGCATTTATGATTTA 249  
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DB 48 LeuAsnProIleValLeuProGluTYrLeuIleHisAlaPhePheCysValMetPheLeu 67  
QY 250 TATTTTAAATGATTTAGGTTTGTGGCTGAGTACTGAAATAAC-----AGT 297  
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DB 68 -----CysAlaAlaGluTrpLeuThrLeuGluLeuAsnMetProIleuLeuAla 83  
QY 298 GAGCATATCTGG--TATATGTCA----- 318  
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DB 84 TYRHisIleTrpArgTYrMetSerArgProValMetSerGlyProGlyLeuTYrAspPro 103  
QY 319 TTTATTATGTTAAATTACATTTTAAAGTCATGTCATATAAGGTATGAAACATAT 378  
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DB 104 ThrThrIleMetAsnAlaAspIleLeuAlaTYrCysGlnLYSGluGlyTrp----- 120  
QY 379 CATGTTAATGACAGATGCAAGTTA--TTTATTGCTTATTTT 420  
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DB 121 -----CysLYSLeuAlaPheTYrLeuLeuAlaPhe 130

RESULT 14

US-09-978-192A-322  
Sequence 322, Application US/09978192A  
Patent No. US2002017553A1

GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Bacon, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Goddard, Audrey E.

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Paoni, James

APPLICANT: Paoletti, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tunas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: secreted and transmembrane Polypeptides and Nucleic

FILE REFERENCE: P2630PIC9

CURRENT FILING DATE: 2001-07-10

NUMBER OF SEQ ID NOS: 2001-07-10

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 327

LENGTH: 144

TYPE: PRT

ORGANISM: Homo sapiens

US-09-902-941-327

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PRIOR APPLICATION NUMBER:	60/085322

Tue Nov 23 09:18:27 2004

us-09-705-500a-1.rapb

Page 11

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; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 3 68 length: 144
Score: 75.00 Matches: 13
Percent Similarity: 41.74% Conservative: 33
Best Local Similarity: 28.70% Mismatches: 27
Query Match: 8.58% Indels: 40
DB: 9 Gaps: 9

US-09-705-500a-1 (1-503) x US-09-978-192a-322 (1-144)
QY 142 CTGACAGTGATTCGGGGGCTGACCTAGACCACTTGATTCCTCTGATTTG 201
Db 34 LeuLysThrAspTyrLysAsnProLleAspGln-----CysAsnTr 47
QY 202 -----GTGACCTTAGACATTTTGTGCCAT---TATATTGACATTAGTATTA 249
Db 48 LeuAsnProLeuValLeuProGluTyrLeuIleHisAlaPheheCysValheCpneu 67
QY 250 TAAATTAATGATATTTAGTTTGGCTGAGTACTGGAATAAAC-----AGT 297
Db 68 -----CysAlaIaGluTrpLeuThrLeuGlyLeuAsnheCProLeuAla 83
QY 298 GAGCATATCTG---TATATGCA----- 318
Db 84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103
QY 319 TTATTTATTTGTTAATTAATTCATTTTAACTCCATGTCATATTAAGTTATGAACATAT 378
Db 104 ThThrIleMetAsnAlaAspIleLeuAlaTyrCysGlnLysGluGlyTrp----- 120
QY 379 CATGTATATGACAGATGCAAGTTA---TTTATTTGCTTATTTT 420
Db 121 -----CysLysLeuAlaPheTyrLeuAlaIahe 130

RESULT 15
US-09-999-832a-322
; Sequence 322, Application US/09999832A
; Publication No. US20020192706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gertsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gunney, Austin L.
; APPLICANT: Hillan, Kenneth J
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C63
; CURRENT APPLICATION NUMBER: US/09/999,832A
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: 09/918585
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PRIOR FILING DATE: 1998-05-15  
PRIOR APPLICATION NUMBER: 60/085580  
PRIOR FILING DATE: 1998-05-15  
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Alignment Scores:  
Pred. No.: 3.68 Length: 144  
Score: 75.00 Matches: 33  
Percent Similarity: 41.74% Conservative: 15  
Best Local Similarity: 28.70% Mismatches: 27  
Query Match: 8.58% Indels: 40  
Gaps: 9

US-09-705-500A-1 (1-503) x US-09-999-832A-322 (1-144)

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34 LeuylsThrsprylzylsAsnProIleAspGln-----CysAsnThr 47  
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202 -----GTGCACCTTTAGACATTTTGTGCAAT---TATATTGCATTAATGATTA 249  
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48 LeuAsnProIleuValLeuProGluTyrLeuIleHisAlaIleAspHehCysValMetProIleu 67  
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250 TAAATTAATGATATTTAGGTTTGGCTGAGTACTGATTAATAAC-----AGT 297  
68 -----CysAlaAlaGluTrpLeuThrLeuGlyLeuAsnMetProIleuLeuAla 83  
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298 GAGCATATCTGG---TATATGTCA----- 318  
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84 TyrHisIleTrpArgTyrMetSerArgProValMetSerGlyProGlyLeuTyrAspPro 103  
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Search completed: November 22, 2004, 18:05:27  
Job time : 277.5 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 22, 2004, 10:37:26 ; Search time 79 Seconds  
(without alignments)

4525.656 Million cell updates/sec

Title: US-09-705-500A-1  
Perfect score: 503  
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	48	9.5	1141	4 US-09-806-708B-22	Sequence 22, Appl
4	48	9.5	640681	4 US-09-790-988-1	Sequence 1, Appl
5	47.8	9.5	1286	4 US-09-601-198-154	Sequence 154, Appl
6	46.4	9.2	6508	4 US-09-995-917A-2	Sequence 2, Appl
7	45.6	9.1	6669	4 US-10-204-708-6	Sequence 6, Appl
8	45	8.9	6801	4 US-10-204-708-61	Sequence 61, Appl
9	44	8.7	4383	6 5175095-4	Patent No. 5175095
10	43.4	8.6	1988	3 US-09-402-002-3	Sequence 3, Appl
11	43.2	8.6	19233	4 US-10-204-708-45	Sequence 45, Appl
12	42.8	8.5	10467	4 US-10-204-708-2	Sequence 2, Appl
13	42.8	8.5	6317	4 US-10-204-708-12	Sequence 12, Appl
14	42.8	8.5	10640	4 US-09-417-485D-5	Sequence 5, Appl
15	41.8	8.3	7304	4 US-10-204-708-43	Sequence 43, Appl
16	41.8	8.3	640681	4 US-09-790-988-1	Sequence 1, Appl
17	41.4	8.2	687	4 US-09-248-796A-8427	Sequence 8427, Ap
18	41.4	8.2	5610	4 US-10-204-708-54	Sequence 54, Appl
19	41.4	8.2	8093	4 US-10-204-708-32	Sequence 32, Appl
20	41.4	8.2	9347	4 US-10-204-708-35	Sequence 35, Appl
21	41.4	8.2	19124	2 US-08-487-826B-13	Sequence 13, Appl
22	41.4	8.2	19513	4 US-10-204-708-39	Sequence 39, Appl
23	41.2	8.2	5152	4 US-10-204-708-73	Sequence 73, Appl
24	41.2	8.2	19233	4 US-10-204-708-46	Sequence 46, Appl
25	41	8.2	8607	4 US-10-204-708-71	Sequence 71, Appl
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C 28	40.4	8.0	618	3 US-08-953-326-22	Sequence 22, Appl
C 29	40.4	8.0	618	4 US-09-553-662-22	Sequence 22, Appl
C 30	40.4	8.0	618	4 US-10-062-994-32	Sequence 22, Appl
31	40.4	8.0	5476	4 US-10-204-708-82	Sequence 82, Appl
32	40.4	8.0	5562	4 US-10-204-708-63	Sequence 63, Appl
33	40.4	8.0	6156	4 US-10-204-708-60	Sequence 60, Appl
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36	40	8.0	660	2 US-08-544-332-32	Sequence 32, Appl
37	40	8.0	660	4 US-09-370-861A-32	Sequence 32, Appl
38	40	8.0	1511	1 US-07-991-867B-8	Sequence 8, Appl
39	40	8.0	1511	1 US-08-107-755A-8	Sequence 8, Appl
40	40	8.0	1511	2 US-08-544-332-8	Sequence 8, Appl
41	40	8.0	1511	4 US-09-370-861A-8	Sequence 8, Appl
42	40	8.0	4810	3 US-08-852-629-11	Sequence 11, Appl
43	40	8.0	4838	3 US-08-852-629-15	Sequence 15, Appl
44	40	8.0	8961	4 US-10-204-708-80	Sequence 80, Appl
45	40	8.0	11049	4 US-10-204-708-22	Sequence 22, Appl

#### ALIGNMENTS

RESULT 1  
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Sequence 1502, Application US/09023655  
Patent No. 6607879  
GENERAL INFORMATION:  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Susan G. Stuart  
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
TITLE OF INVENTION: EXPRESSION  
NUMBER OF SEQUENCES: 1508  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/023,655  
FILING DATE: HERMITH  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Zeller, Karen J.  
REGISTRATION NUMBER: 37,071  
REFERENCE/DOCKET NUMBER: PA-0001 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 855-0555  
TELEFAX: (650) 845-4166  
INFORMATION FOR SEQ ID NO: 1502:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3757 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: 9975297  
US-09-023-655-1502  
Query Match 91.1%; Score 458; DB 4; Length 3757;





QY 65 TAGTTTTTGCTCTCTCTTCCCTCCACCGCTACCTCCCAATTCGCCCTTAAACCTCCAAA 124  
 Db 715 NNAAGTAKNNNNNNNAGAGAAAKKYYAAAAAYKAAKEHRRANKRAMEGMDADAAETTDKRN 774  
 QY 125 GCTTCGCTCTGTGTGTGTGTCGACAGAGTGAATCGGGGGCTGACCTAGACAGTTGGCATGAT 184  
 Db 775 GAYTKYTTNNNNNYTGVVYTTAAADGWAANNNNNNNNNNNNNGMSDMVYTWMAVANYGT 834  
 QY 185 TCTTCCTCTGTGATTTGGTGTGACCTTGAACATTTTGTGCATTAATTTGGATTAATG 244  
 Db 835 NNNNNNNNNNAYAAWWTNKWY--YTTDRMBRAYNNNNNNNNNNNNKAYGAYVADDDAYWSDT 891  
 QY 245 ATTATTAATTTAAATATATATTTAGGTTTTTGGCTGAGTACGAGATTAACAGTGAGCAT 304  
 Db 892 CDAMEMMDATKNNNNATNTYRGTAMTNNNNNNMMTKTYEHAAMNNNNNNNGKCAHTW 951  
 QY 305 TCTGTATATATGTCATTATTATTGTTAAATTAACATTTTAAAGCTTCATGCGCATATAAG 364  
 Db 952 WVCATKTKTKGCMNCCCTYCRXYKNNCCWYTWMTTRCTYTAARMKXNNATSGMTRCA 1011  
 QY 365 GTTATGAACATATCATCTGTAATGACAGATGCAAGTTATTATTATTTGTTATTATTA 424  
 Db 1012 TGMKNNNNYTGWKTRTATYRMAATRRMKAKWKMAIGSNNTSYAPMAKTRAYKGYTNA 1071  
 QY 425 TTAAGATGTCATGACATATATGAAGCCTTGGTGAATTCCTCTAAGATAAAATAAT 484  
 Db 1072 CARMRMGKATCTMTDNAMWTTACATSMWATHKXNMHWCKNNNNNNNNNTMRAVAAAAN 1131  
 QY 485 AATTA 489  
 Db 1132 CDGAR 1136  
  
 RESULT 4  
 US-09-790-988-1  
 ; Sequence 1, Application US/09790988  
 ; Patent No. 6632935  
 ; GENERAL INFORMATION  
 ; APPLICANT: SHIGENOBU, SHUJI  
 ; APPLICANT: MATSANBE, HIDEKI  
 ; APPLICANT: HATTORI, MASAHIRA  
 ; APPLICANT: SAKAKI, YOSHITOKI  
 ; TITLE OF INVENTION: GENOME DATA OF BACTERIAL SYMBIONT OF APHIDS  
 ; FILE REFERENCE: 081356/0159  
 ; CURRENT APPLICATION NUMBER: US/09/790,988  
 ; PRIOR FILING DATE: 2001-02-23  
 ; PRIOR APPLICATION NUMBER: JP2000-107160  
 ; NUMBER OF SEQ ID NOS: 7  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 1  
 ; LENGTH: 640681  
 ; TYPE: DNA  
 ; ORGANISM: Buchnera sp.  
 US-09-790-988-1

Query Match	9.5%;	Score	48;	DB	4;	Length	640681;
Best Local Similarity	50.9%;	Prod.	No. 0.037;				
Matches	114;	Conservative	0;	Mismatches	110;	Indels	0;
Gaps	0;						
Qy	198	TTTGGTTGCACCTTAAGACATTTTGTGTCATTATAATTTGCATTATGATATTAATTAATTTAA	257				
Db	325119	TTTATTTAATTAATTAACCTAATTTTATTCATTTTATTAATTTTAAATTTTAAAAAATTT	325178				
Qy	258	ATGATATTAGGTTTTTGGCTGACCTCGAATAAGCTGAGCATATCTGGTATATGTC	317				
Db	325179	TCTTAAATTAATTAATTTTAAATGATGATTTAAATAAATAATTAATTAATTTTATTTTATTTT	325238				
Qy	318	ATTATTTATTTGTTAAATTTACATTTTTCAGCTGCATGTGATATAAAGGTTATGAACATA	377				
Db	325239	ACATTTATTTATTAATTAATAAATTTTACTATAAATAATTTTAAATTTTAAATAAATAACATT	325298				
Qy	378	TCATGTGAATGACAGATGCAAGTATTTATTTTGGCTATTTTAA	421				

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Db          325299  TATATATAATAAATACTGATATTTCTTTCTTTATATTTTATA 325342

      RESULT 5
      ; Sequence 154, Application US/09601198
      ; Patent No. 6531583
      ; GENERAL INFORMATION:
      ; APPLICANT: Cassell, Gail H.
      ; APPLICANT: Chen, Ellison Y.
      ; APPLICANT: Glass, Jennifer S.
      ; APPLICANT: Glass, John I.
      ; APPLICANT: Heiner, Cheryl R.
      ; APPLICANT: Lefkowitz, Elliot
      ; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
      ; TITLE OF INVENTION: UREALYTICUM
      ; FILE REFERENCE: UAB-13452/22
      ; CURRENT APPLICATION NUMBER: US/09/601,198
      ; CURRENT FILING DATE: 2000-12-08
      ; PRIOR APPLICATION NUMBER: 60/073,189
      ; PRIOR FILING DATE: 1998-01-30
      ; NUMBER OF SEQ ID NOS: 181
      ; SOFTWARE: PatentIn Ver. 2.0
      ; SEQ ID NO 154
      ; LENGTH: 1296
      ; TYPE: DNA
      ; ORGANISM: Ureaplasma urealyticum
US-09-601-198-154

```

```

RESULT 6
US-09-995-917A-2/c
; Sequence 2, Application US/0995917A
; Patent No. 6768043
; GENERAL INFORMATION:
; APPLICANT: MANG
; TITLE OF INVENTION: DASS, A P450 PROTEIN INVOLVED IN THE
; TITLE OF INVENTION: BRASSINOSTEROID BIOSYNTHESIS PATHWAY IN PLANTS
; FILE REFERENCE: SALKINS.045A
; CURRENT APPLICATION NUMBER: US/09/995,917A
; CURRENT FILING DATE: 2001-11-27
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 6508
; TYPE: DNA
; ORGANISM: DASS
US-09-995-917A-2

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	Query Match	Similarity	Score	DB	Length
Best Local	50.3%	Pred. No. 0.021;			
Matches	145;	Conservative	0;	Mismatches	135;
				Indels	7;
				Gaps	1;

  

	Query Match	Similarity	Score	DB	Length
Best Local	47.0%	Pred. No. 0.034;			
Matches	173;	Conservative	0;	Mismatches	194;
				Indels	1;
				Gaps	1;

Oy	316	TCATTATTATTATGTTAAATTAACATTTTTAAAGTCACATGTCATTAAGTTAAGTTATGAACA	375
Db	6147	ATTTTATTATTATTTTGTGTTTGTATATAGTAATTTGTGTAATATATTTTATTATTTTAA	6206
Oy	376	TATCATGTGTAATGACAGATGCAAGTATTTTATTGCTTATTTTATATTAATTAAGATGCC	435
Db	6207	GTAATATGTAAATTTTATAGATAGAAATTTGTTTGTATTTGTGTGATTTAGTAATATA	6266
Oy	436	ATAGCATAAATATGGAAGCCTTTGGTGA-ATTCCTCTAAGATTAANAATATATATTAAGT	494
Db	6267	AGATAATATTAAGTAGCGTTTTTTAAAGATTTATTGTATGTTTAAAGAAATTAATATAT	6326
Oy	495	TACGTTT 502	
Db	6327	TAAATTTT 6334	
RESULT 8			
US-10-204-708-61			
Sequence 61, Application US/10204708			
Patent No. 6677731			
GENERAL INFORMATION:			
APPLICANT: OLEK, Alexander			
APPLICANT: PIERENBROCK, Christian			
APPLICANT: BERLIN, Kurt			
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication			
FILE REFERENCE: 5013.1012			
CURRENT APPLICATION NUMBER: US/10/204, 708			
CURRENT FILING DATE: 2003-05-06			
PRIOR APPLICATION NUMBER: PCT/EP01/03971			
PRIOR FILING DATE: 2001-04-06			
PRIOR APPLICATION NUMBER: DE 10019058.8			
PRIOR FILING DATE: 2000-04-06			
PRIOR APPLICATION NUMBER: DE 10019173.8			
PRIOR FILING DATE: 2000-04-07			
PRIOR APPLICATION NUMBER: DE 10032529.7			
PRIOR FILING DATE: 2000-06-30			
PRIOR APPLICATION NUMBER: DE 10043826.1			
PRIOR FILING DATE: 2000-09-01			
NUMBER OF SEQ ID NOS: 98			
SEQ ID NO 61			
LENGTH: 6801			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)			
US-10-204-708-61			
Query Match			
Best Local Similarity 52.9%; Score 45; DB 4; Length 6801;			
Matches 119; Conservative 0; Mismatches 105; Indels 1; Gaps 1;			
Oy	209	TTTAGACATTTTGTGCGCATTTATATTTGCAATTAATGATTAATTAATTAATTAAGATTAG	268
Db	6390	TTTATATATTTAGAGTTAAATTTATATATATAGTATATTTTATTATTAGTTTTTTTG	6449
Oy	269	GTTTTGGCTGAGTACTGGAATPAACAGTAGACATATCTGATATGTCATTAATTATG	328
Db	6450	ATTTTTTTTGTGTTTTGTGTTTTAGGGTAGAGGTGTATATATTTTATTTTAGGTG	6509
Oy	329	TTAAATACATTTTAAAG-CTCATGTGCATATPAAGGTATGAAACATATCATGTGAAT	387
Db	6510	TTATTTTAAATTTTAAATTTGATGATTTTGTGATATTTTATATATATATATATATAT	6569
Oy	388	GACAGATGAAGTATTTTATTTGCTTATTTTATATTAATTAAGAT 432	
Db	6570	TGTGAATAGATGTTGTTTATTTTATTTTATTTTATTTTATGTT 6614	
RESULT 9			
US-10-204-708-61			

RESULT 10  
 US-09-402-002-3/c  
 : Sequence 3, Application US/09402002  
 : Patent No. 6225453  
 :  
 : GENERAL INFORMATION:  
 : APPLICANT: Ueyama, Hiroshi  
 : APPLICANT: Abe, Kanako  
 : APPLICANT: Keshi, Hiroyuki  
 : APPLICANT: Matsushita, Akio  
 : TITLE OF INVENTION: PROBES FOR THE DIAGNOSIS OF INFECTIONS  
 : TITLE OF INVENTION: CAUSED BY KLEBSIELLA PNEUMONIAE  
 :  
 : NUMBER OF SEQUENCES: 7  
 :  
 : CORRESPONDENCE ADDRESS:  
 : ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Bortun  
 : STREET: 233 South Wacker Drive/6300 Sears Tower  
 : CITY: Chicago  
 : STATE: Illinois  
 : COUNTRY: United States of America  
 : ZIP: 60606  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/09/402, 002  
 : FILING DATE:  
 : CLASSIFICATION: 435  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: JP 1997-71082  
 : FILING DATE: 25-MAR-1997  
 :  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: PCT/JP98/01286  
 : FILING DATE: 23-MAR-1998  
 :  
 : ATTORNEY/AGENT INFORMATION:  
 : NAME: Cawley, Jr., Thomas A.  
 :  
 : REGISTRATION NUMBER: 40,944

QY	228	TTTATTTTCATTTATGATTTATTTAAATTTAAATGATTTAGCTTTTGGCTGAGTACTGG	287
Db	206	TCACTTATTTCTCCTTTGTTCTTCCTTCATTTATTTAATGACATAATTAATATTGT	147
QY	288	AATPAAACAGTGACATATCTGGTATATGTCATTTATTTATGGTAAATTAACAATTTTAAAC	347
Db	146	CAATATATTTATACACATCTTGACATATTTAATATTGTTGTATTTATTATATAGTAAC	87
QY	348	TCCATGTGCATTTAAAGTTATGAAACATATCAGTGATATGACAGATGCAAGTTATTTTA	407
Db	86	CAATTTAAATATATAGATAGGAAACAAATPAAACATTCACAAATATGAGAAAGTATGAG	27
QY	408	TTTGCTTATTTTATATATPAAAGAT	432
Db	26	AGCAAAATCTTTTATTTCTAGCT	2

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RESULT 11
US-10-204-708-45
; Sequence 45, Application US/10204708
; Patent No. 6677721
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 45
; LENGTH: 19233
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:

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NAME/KEY: unsure
LOCATION: (76, 178..179, 273, 586, 648, 651, 920, 1014, 1173, 1197, 1228)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (1264, 1267, 1559, 1607, 1677, 1703, 1742, 1848, 1850, 2033)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (2168, 2254, 2257, 2280, 2291, 2723, 3018, 3080, 4205, 4209)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4216, 4225, 4239, 4246, 4254, 4265, 4270, 4274, 4288, 4294..4295)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4298, 4363, 4610, 4627, 4675, 4693, 4698, 4738, 4777, 4781)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (4787, 4825, 4829, 4838, 4855, 5462, 5494, 5496, 5500, 5674)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (5690, 5697, 5705, 5715, 5890, 5910, 5913, 6027, 6080, 6109)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (6244, 6288, 6776, 6873, 6891, 6980, 7028, 7656, 7876, 8030)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (8059, 8075, 8632, 8636, 9700, 9717, 9815, 9818, 9867, 9879)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (1005, 10075, 10150, 10159, 10165, 10356, 11123, 11166, 11360)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (11703, 11933, 12050, 12340, 12981, 13564, 13764..13765, 13787)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (13846, 14168, 16566, 17006, 17217, 17650, 17653, 17656, 17898)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (18130, 18143, 18151, 18188, 18498, 18549, 18936, 18946, 19165)
OTHER INFORMATION: n is a or g or c or t
FEATURE:
NAME/KEY: unsure
LOCATION: (19200)
OTHER INFORMATION: n is a or g or c or t
US-10-204-708-45
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Query Match 8.6%; Score 43.2; DB 4; Length 19233;
Best Local Similarity 47.5%; Pred. No. 0.19;
Matches 150; Conservative 0; Mismatches 164; Indels 2; Gaps 1;
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QY 175 TTTCGATGATCTCTCTGATTTGGTGCATTTAGACATTTTGTGCTATTTAT 234
DB 1588 TTTCGATTTATGTTTTTTTGTGTTAGTTTTTTTATTTATTTAGTTATTTAT 1647
QY 235 TGCAATTAGTATTATTAATTAATGATATTAGTTTTGGCTGAGTACTGGAATTAAC 294
DB 1648 GTGATATTATTATTTATTTGATTTGGGNTTTGGGTTTGAATTTTGATTTTAA 1707
QY 295 AGTGAGATATCTGCTATGTCATTTATTTATTTAAATTAATTTTAAAGTCCAGT 354
DB 1708 TTTAAAGTCGTTTTTTTAAAGTTATTTGAATTTGATTTTAAATTTATTTAGT 1767
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QY 355 GCATTAAGTTATGAAACATA--TCATGTTATGACAGATGCAAGTTATTTATTCG 412
DB 1768 TAGATATATGTTAGGATGATGTTTACCTTTGATTTTGTGATTTTGGATGTTGG 1827
QY 413 TTATTTTATTAATTAAGATGCCATATGATATGAGCCTTTGGTGAATTCCTCTAA 472
DB 1828 GGATTTATTTAGATTTGAGATTTTATGTTAGTTGTTAAATCGGTGAATTTTATTT 1887
QY 473 GATTAATTAATTAATA 488
DB 1888 TATTAATTAATTAATAA 1903
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RESULT 12
US-10-204-708-2
```

```
; Sequence 2, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIRENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 2
; LENGTH: 10467
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-2
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Query Match 8.5%; Score 43; DB 4; Length 10467;
Best Local Similarity 49.3%; Pred. No. 0.18;
Matches 112; Conservative 0; Mismatches 115; Indels 0; Gaps 0;
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QY 216 ATTTTGGCATTAATTTGCAATTAATTAATTAATTAATTAATTAATTAATTTAGTTTTG 275
DB 478 ATTTTTTTATAGTTAGTTATTTAGTTATTTTGTGTTATTTGTTTAAAGATTTATC 537
QY 276 GCTAGTACTGGAATTAACAGTGCATCTGATCTGATATGCTATTTATTTGTTAAAT 335
DB 538 GTTTAGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTAGTTTTT 597
QY 336 ACATTTTAAAGCTCATGTCATTAAGCTTAATTAATTAATTAATTAATTAATTAATTA 395
DB 598 AAGTTGTAATAGCTGATGAAGAAATTAATTTTATTTAGTGGAAATAGCTTACGGAATTT 657
QY 396 CAAGTATTTATTTGCTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAAT 442
DB 658 AGAGTATTTTGTGTTTTTATTTATTTATTTAGGAGATTTAGAT 704
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RESULT 13
US-10-204-708-12
; Sequence 12, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIRENBROCK, Christian
```

```

; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: US/10/204,708
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 12
; LENGTH: 6317
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-12

Query Match
Best Local Similarity 8.5%; Score 42.8; DB 4; Length 6317;
Matches 142; Conservative 0; Mismatches 147; Indels 1; Gaps 1;

QY 205 GCACTTTAGACATTTTGTGCGCATTTATATTGCAATTATGATTTAATTAATGATAT 264
DB 473 GAAGTTAGAAATATGTAATAAATGAATGATGCTTTTATAGTATTATTAAGTTGT 532
QY 265 TTAGCTTTTGGCTGAGTACTGCAATTAACAGTACGACATCTCGTATATGTCATTA 324
DB 533 ATTTTAAATGATGATGTTTGTGTTTAAAGAGTTGTTATATATATGTTTAAATTT 592
QY 325 ATGTTAAATTAACATTTTAAAGCTCCATGTCATATA-AAAGTTAAGAAACATCATGG 383
DB 593 AGTTTAAAGATGTAATAAAGTTATTTTGAATGAGAAATGAAACGTTAAATTA 652
QY 384 TAATGACAGATGCAAGTATTTTATTTGCTTATTTTATTAATTAAGATCCATAGCATA 443
DB 653 TTTCGAGACCTATTTGTTATATATTTGTTTATTAATTAATTAAGTGAAGTAAAGAT 712
QY 444 ATATGAAGCCTTTGGTGAATTCCTCTAGATATAAATAATATAAGTG 493
DB 713 ATATTTTAAAGCGTTTATATTTTATTTATGAGGAGAAAGTTATTTTG 762

RESULT 14
US-09-417-485D-5/c
; Sequence 5, Application US/09417485D
; Patent No. 6541202
; GENERAL INFORMATION:
; APPLICANT: Long, David M.
; APPLICANT: Metz, Anneke M.
; APPLICANT: Love, Ruschelle A.
; TITLE OF INVENTION: Telomerase Reverse Transcriptase (TERT) Genes
; FILE REFERENCE: 47714-5009-US
; CURRENT APPLICATION NUMBER: US/09/417,485D
; CURRENT FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10640
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (834)..(7385)
; OTHER INFORMATION: TERT gene
; FEATURE:
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; NAME/KEY: unsure
; LOCATION: (1821)..(1837)
; OTHER INFORMATION: n at position 1821 = a or c; w at position 1837 =
; OTHER INFORMATION: a or c. Xaa (amino acid) at position 330 = Leu or
; OTHER INFORMATION: Ile; Xaa at position 335 = Asp or Gly.
US-09-417-485D-5

Query Match
Best Local Similarity 8.5%; Score 42.8; DB 4; Length 10640;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 184 TTCTTCTCTGATTTGGTGGCACTTATAGACATTTTGGCATTAATTTGCATTATG 243
DB 2841 TTTTATTTATTAATTTTATTTTATGTTATCATTTATTTTATGATTTCTTATTA 2782
QY 244 TATTATATTTAATGATATTTAGTTTGGCTGAGTACGGAATTAAGTAGCAT 303
DB 2781 TATGTAATTTTGTTCATAGTTGTTATCAATATATTTCTTAATAAATTCATAT 2722
QY 304 ATCTGATATGTCATTTATTTATTTGTTAAATTAATTTTAAAGTCCATGTCATATA 363
DB 2721 TTAATTTATTTACTTATTTTATTTTGAATATATTTTAACTTATATTTTCATTA 2662
QY 364 GGTATGAACATATCATGATGATGACAGATGCAAGTATTTTATTTGCTTATTTTATA 423
DB 2661 CTGATTTAGCAAAACCTTCTTATATTAATTAATTAACAAAATTTTATACATTTT 2602
QY 424 ATTAAA 429
DB 2601 AAAATA 2596

RESULT 15
US-10-204-708-43
; Sequence 43, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: Oler, Alexander
; APPLICANT: PIERENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 43
; LENGTH: 7304
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-43

Query Match
Best Local Similarity 8.3%; Score 41.8; DB 4; Length 7304;
Matches 152; Conservative 0; Mismatches 162; Indels 3; Gaps 1;

QY 187 TTCTCTTGTGATTTGGTGAACCTTATAGACATTTTGTGCAATTAATTTGCATTATG 246
DB 515 TTGAGTTTATTTTGTGCGTTAGGTTGAGATATAGGTTATATATATCGGTTTATG 574
QY 247 TTATATTTAATGATATTTAGGTTTGGCTGAGTACTGGAATTAACAGTGAACATATC 306
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